```
Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
             ||      ||||||||||||||||||||
Db       1383 TGATTGTGAAAAAAAAAAAAAAAAAA 1409


RESULT 210
AAZ65261
ID   AAZ65261 standard; DNA; 1447 BP.
XX
AC   AAZ65261;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Human secreted protein gene 12.
XX
KW   Human; secreted protein; cancer; tumour; developmental abnormality;
KW   foetal deficiency; blood disorder; immune system disorder; inflammation;
KW   autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW   schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW   atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW   digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW   therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO9958660-A1.
XX
PD   18-NOV-1999.
XX
PF   06-MAY-1999;   99WO-US009847.
XX
PR   12-MAY-1998;   98US-0085093P.
PR   12-MAY-1998;   98US-0085094P.
PR   12-MAY-1998;   98US-0085105P.
PR   12-MAY-1998;   98US-0085180P.
PR   18-MAY-1998;   98US-0085906P.
PR   18-MAY-1998;   98US-0085920P.
PR   18-MAY-1998;   98US-0085921P.
PR   18-MAY-1998;   98US-0085922P.
PR   18-MAY-1998;   98US-0085923P.
PR   18-MAY-1998;   98US-0085924P.
PR   18-MAY-1998;   98US-0085925P.
PR   18-MAY-1998;   98US-0085927P.
PR   18-MAY-1998;   98US-0085928P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Florence K,  Ni J,  Rosen CA,  Carter KC,  Moore PA;
PI   Olsen HS,  Shi Y,  Young PE,  Wei F,  Brewer LA,  Soppet DR,  Lafleur DW;
PI   Endress GA,  Ebner R;
XX
DR   WPI; 2000-062296/05.
DR   P-PSDB; AAY76135.
XX
PT   New isolated human genes and the secreted polypeptides they encode,
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Claim 1; Page 303; 475pp; English.
XX
CC   AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC   AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC   human genes. The genes and their corresponding secreted polypeptides are
CC   useful for preventing, treating or ameliorating medical conditions, e.g.
CC   by protein or gene therapy. Also pathological conditions can be diagnosed
CC   by determining the amount of the new polypeptides in a sample or by
CC   determining the presence of mutations in the new genes. Specific uses are
CC   described for each of the 97 genes, based on which tissues they are most
CC   highly expressed in, and include developing products for the diagnosis or
CC   treatment of cancer, tumours, developmental abnormalities and foetal
CC   deficiencies, blood disorders, diseases of the immune system, autoimmune
CC   diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC   schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
```

CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.4%; Score 1324.6; DB 3; Length 1447;
Best Local Similarity 99.3%; Pred. No. 3.5e-258;
Matches 1338; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |     ||||||||||||||||||||
Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAA 1417
```

RESULT 211
ADE11650
ID ADE11650 standard; cDNA; 1447 BP.
XX
AC ADE11650;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted polypeptide cDNA #12.
XX
KW Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
KW Alzheimer's disease; human; ss; gene.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003100051-A1.
XX
PD 29-MAY-2003.
XX
PF 10-SEP-2001; 2001US-00948783.
XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
PR 06-MAY-1999; 99WO-US009847.
PR 10-NOV-1999; 99US-00437658.
PR 11-SEP-2000; 2000US-0231846P.
PR 28-JUN-2001; 2001US-00892877.
XX
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.

RESULT 212
AAZ65261
ID AAZ65261 standard; DNA; 1447 BP.
XX
AC AAZ65261;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human secreted protein gene 12.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9958660-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009847.
XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R;
XX
DR WPI; 2000-062296/05.
DR P-PSDB; AAY76135.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 303; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed

CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 97 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.2%; Score 626.6; DB 3; Length 1447;
Best Local Similarity 99.7%; Pred. No. 3.6e-181;
Matches 637; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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Qy        1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       77 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 136

Qy       61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy      121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy      181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy      241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy      301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db      377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy      361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy      421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      497 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 556

Qy      481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy      541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy      601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
          |||||||||||||| |||||||||||||||||||||||||
Db      677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 715
```

RESULT 213
ADE11650
ID ADE11650 standard; cDNA; 1447 BP.
XX
AC ADE11650;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted polypeptide cDNA #12.

PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
XX
PI Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R, Birse CE;
XX
DR WPI; 2003-801210/75.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX
PS Claim 1; SEQ ID NO 22; 453pp; English.
XX
CC The invention relates to human secreted polypeptides and the
CC polynucleotides encoding them. The sequences are useful for preparing
CC medicaments for preventing, treating or ameliorating medical conditions
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC as Alzheimer's disease. This sequence represents cDNA encoding a human
CC secreted polypeptide of the invention.
XX
SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.4%; Score 1324.6; DB 9; Length 1447;
Best Local Similarity 99.3%; Pred. No. 3.5e-258;
Matches 1338; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAGGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              ||  |  ||||||||||||||||||||
Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAAA 1417
```

RESULT 212
AAV40540
ID AAV40540 standard; cDNA; 1401 BP.
XX
AC AAV40540;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens secreted protein clone AM42_3.
XX
KW Clone; secreted protein; ds.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 71. .739
FT /*tag= a
FT /note= "secreted protein"
XX
PN WO9832853-A2.
XX
PD 30-JUL-1998.
XX
PF 23-JAN-1998; 98WO-US001396.
XX
PR 24-JAN-1997; 97US-00788789.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-427949/36.
DR P-PSDB; AAW29670.
XX
PT New isolated polynucleotide(s) and secreted proteins - isolated from
PT human foetal kidney, adult brain, adult salivary gland, foetal brain and
PT adult testes cDNA libraries.
XX
PS Claim 16; Page 64-65; 109pp; English.
XX
CC The sequence is that of encoding a secreted protein. Such a protein can
CC have biological activities, e.g. nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity, and other activities
XX
SQ Sequence 1401 BP; 458 A; 258 C; 251 G; 434 T; 0 U; 0 Other;

Query Match 98.2%; Score 1321.8; DB 2; Length 1401;
Best Local Similarity 99.8%; Pred. No. 1.3e-257;
Matches 1334; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db   65 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 124

Qy   61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db  125 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 184

Qy  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db  185 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 244

Qy  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db  245 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 304

Qy  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db  305 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 364

Qy  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db  365 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTA 424

Qy  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db  425 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 484

Qy  421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db  485 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 544

Qy  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db  545 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 604

Qy  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db  605 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 664

Qy  601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
Db  665 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 724

Qy  660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
Db  725 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 784

Qy  720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
Db  785 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 844

Qy  780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
Db  845 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 904

Qy  840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
Db  905 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 964

Qy  900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
Db  965 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1024

Qy  960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
Db 1025 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1084

Qy 1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
Db 1085 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1144

Qy 1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
Db 1145 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1204

Qy 1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
Db 1205 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1264

Qy 1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
Db 1265 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1324

Qy 1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
Db 1325 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1384

Qy 1320 TAAAAAAAAAAAAAAAA 1336
Db 1385 AAAAAAAAAAAAAAAAA 1401
```

RESULT 213
AAF94470
ID AAF94470 standard; cDNA; 1347 BP.
XX
AC AAF94470;
XX
DT 04-JUN-2001 (first entry)
XX
DE Human hydrophobic domain containing protein clone HP10720 cDNA #84.
XX

```
Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 623

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        624 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 662
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RESULT 215
AAV40540
ID AAV40540 standard; cDNA; 1401 BP.
XX
AC AAV40540;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens secreted protein clone AM42_3.
XX
KW Clone; secreted protein; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 71. .739
FT /*tag= a
FT /note= "secreted protein"
XX
PN WO9832853-A2.
XX
PD 30-JUL-1998.
XX
PF 23-JAN-1998; 98WO-US001396.
XX
PR 24-JAN-1997; 97US-00788789.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-427949/36.
DR P-PSDB; AAW29670.
XX
PT New isolated polynucleotide(s) and secreted proteins - isolated from
PT human foetal kidney, adult brain, adult salivary gland, foetal brain and
PT adult testes cDNA libraries.
XX
PS Claim 16; Page 64-65; 109pp; English.
XX
CC The sequence is that of encoding a secreted protein. Such a protein can
CC have biological activities, e.g. nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity, and other activities
XX
SQ Sequence 1401 BP; 458 A; 258 C; 251 G; 434 T; 0 U; 0 Other;

Query Match 98.0%; Score 625.4; DB 2; Length 1401;
Best Local Similarity 99.7%; Pred. No. 8.3e-181;
Matches 637; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 130

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 190
```

```
Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 250

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 310

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 370

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        371 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTAAATGAC 430

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 490

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 550

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 610

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 670

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        671 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 709
```

RESULT 216
AAX19983
ID AAX19983 standard; cDNA; 848 BP.
XX
AC AAX19983;
XX
DT 16-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO:27.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906439-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001233.
XX
PR 01-AUG-1997; 97US-00904468.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153700/13.
DR P-PSDB; AAY04156.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA

PT libraries derived from liver, lung, large intestine, colon, thyroid and
PT pancreas tissue.
XX
PS Example 28; Page 157-158; 398pp; English.
XX
CC AAX40251 to AAX40397 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY11533 to
CC AAY11679, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC present sequence represents a 5' EST from an example of the present
CC invention
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 217
AAX39430
ID AAX39430 standard; DNA; 848 BP.
XX
AC AAX39430;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO: 27.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906551-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001235.
XX
PR 01-AUG-1997; 97US-00905133.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153781/13.
DR P-PSDB; AAW93620, AAY11373.
XX
PT New nucleic acids encoding human secreted - proteins obtained from cDNA
PT libraries prepared from substantia nigra, cerebellum, surrenals and fetal
PT brain tissue.
XX
PS Example 28; Page 157-158; 434pp; English.
XX
CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY11374 to
CC AAY11531, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. This
CC sequence encodes the human 5' EST secreted proteins represented in
CC AAW93620 and AAY11373
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91
```

```
Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 2
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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RESULT 3
US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 1346
Sequence: 1 gaaagaatgttgtggctgct.....aaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1346	100.0	1346	6	AX403499	AX403499 Sequence
3	1346	100.0	1346	6	AX464348	AX464348 Sequence
4	1346	100.0	1346	9	AY359060	AY359060 Homo sapi
5	1328.6	98.7	1605	9	BC014317	BC014317 Homo sapi
6	1325.4	98.5	1377	9	BC050606	BC050606 Homo sapi
7	1325.4	98.5	1440	9	BC015099	BC015099 Homo sapi
8	1324.6	98.4	1447	6	BD205644	BD205644 97 human
9	1321.8	98.2	1401	6	BD083420	BD083420 Secreted
10	1309.4	97.3	1347	6	AX083392	AX083392 Sequence
11	1307.8	97.2	1345	9	AF229179	AF229179 Homo sapi
12	1305	97.0	1356	6	BD135300	BD135300 110 human

ALIGNMENTS

RESULT 1
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LOCUS AR252633 1346 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 386 from patent US 6478825.
ACCESSION AR252633
VERSION AR252633.1 GI:27300541
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 386 12-NOV-2002;
FEATURES Location/Qualifiers
source 1. .1346
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 1346; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AX403499
LOCUS AX403499 1346 bp DNA linear PAT 14-JUN-2002

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DEFINITION  Sequence 386 from Patent WO0073454.
ACCESSION   AX403499
VERSION     AX403499.1  GI:21436987
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0073454-A 386 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 1346;  DB 6;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2e-266;
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Qy       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
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Qy       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
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Db       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
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Db       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
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Db       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 3
AX464348
LOCUS AX464348 1346 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 481 07-JUN-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 1346; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840
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Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
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Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
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Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
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Db       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

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Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 4
AY359060
LOCUS       AY359060                1346 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION   AY359060
VERSION     AY359060.1  GI:37183237
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1346)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

  Query Match           100.0%;  Score 1346;  DB 9;  Length 1346;
  Best Local Similarity 100.0%;  Pred. No. 2e-266;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Qy        601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660
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Qy        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720
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Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
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Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
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Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
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Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
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Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 5
BC014317
LOCUS BC014317 1605 bp mRNA linear PRI 04-OCT-2003
DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone MGC:22707 IMAGE:4048217), complete cds.
ACCESSION BC014317
VERSION BC014317.1 GI:15680012
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1605)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1605)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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ORIGIN

Query Match 98.7%; Score 1328.6; DB 9; Length 1605;
Best Local Similarity 99.6%; Pred. No. 7.5e-263;
Matches 1342; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 314

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 374

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 434

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 494

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 554

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 614

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 674
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Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        675 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 734

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        735 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 794

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Db        795 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 854

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
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Db        855 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 914

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        975 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 1034

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db       1035 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 1094

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db       1095 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 1154

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Db       1155 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1214

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Db       1215 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1274

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1395 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1454

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1455 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1514

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Db       1515 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTAA 1574

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1575 GTAAAAAAAAAAAAAAAAAAAAAAAA 1601
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RESULT 6
BC050606
LOCUS BC050606 1377 bp mRNA linear PRI 12-NOV-2003
DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone MGC:60059 IMAGE:5183554), complete cds.
ACCESSION BC050606
VERSION BC050606.1 GI:30047080
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1377)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1377)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 110 Row: c Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361864.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="Colon, Kidney, Stomach, adult, whole pooled"
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/lab_host="DH10B"
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SAIRMNKNRINNAFFLNDQTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL
LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAPMTEDER
LTPL"

ORIGIN

Query Match 98.5%; Score 1325.4; DB 9; Length 1377;
Best Local Similarity 99.5%; Pred. No. 3.5e-262;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 62

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 122

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        123 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 182

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 242

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Db        243 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 302

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 362

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        363 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 422

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 482

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        483 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 542

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Db        543 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 602

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Db        603 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 662

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Db        843 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 902

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Db        903 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 962

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1143 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1202

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1323 TGATTGTGAAAAAAAAAAAAAAAAAAAA 1349
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RESULT 7
BC015099
LOCUS BC015099 1440 bp mRNA linear PRI 04-OCT-2003
DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone MGC:22827 IMAGE:3829035), complete cds.
ACCESSION BC015099
VERSION BC015099.1 GI:15929328
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1440)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1440)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

```
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: d Column: 11.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
                      /clone="MGC:22827 IMAGE:3829035"
                      /tissue_type="Kidney, hypernephroma"
                      /clone_lib="NIH_MGC_58"
                      /lab_host="DH10B"
                      /note="Vector: pDNR-LIB"
     gene             1. .1440
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                      /db_xref="LocusID:57393"
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                      NEEYLFKAMVAFSMRKVPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQ
                      SAIRMNKNRINNAFFLNDQTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL
                      LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                      LTPL"
ORIGIN

  Query Match          98.5%;  Score 1325.4;  DB 9;  Length 1440;
  Best Local Similarity  99.5%;  Pred. No. 3.4e-262;
  Matches 1340;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 142

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db        143 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 202

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 262

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 322

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Db        323 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 382

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        383 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 442

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 502

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        503 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 562

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        563 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 622

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 682

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        683 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 742

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Db        743 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 802

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 862

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        863 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 922

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db        923 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 982

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1042

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1102

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1162

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1163 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1222

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1282

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1283 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1342

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1402

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |    ||||||||||||||||||||
Db       1403 TGATTGTGAAAAAAAAAAAAAAAAAAA 1429


RESULT 8
BD205644
LOCUS       BD205644                1447 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  97 human secreted proteins.
ACCESSION   BD205644
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VERSION     BD205644.1  GI:33015414
KEYWORDS    JP 2002533058-A/21.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1447)
  AUTHORS   Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
            Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
            Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
  TITLE     97 human secreted proteins
  JOURNAL   Patent: JP 2002533058-A 21 08-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533058-A/21
            PD   08-OCT-2002
            PF   06-MAY-1999 JP 2000548451
            PR   12-MAY-1998 US    60/085093,12-MAY-1998 US    60/085094 PR
            12-MAY-1998 US    60/085105,12-MAY-1998 US    60/085180 PR
            18-MAY-1998 US    60/085927,18-MAY-1998 US    60/085906 PR
            18-MAY-1998 US    60/085924,18-MAY-1998 US    60/085922 PR
            18-MAY-1998 US    60/085923,18-MAY-1998 US    60/085921 PR
            18-MAY-1998 US    60/085925,18-MAY-1998 US    60/085928 PR
            18-MAY-1998 US    60/085920
            PI   STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH

            PI   C CARTER,
            PI   PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI
            PI   WEI,
            PI   LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A  PI
             ENDRESS,
            PI   REINHARD EBNER
            PC   C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12P21/02,C12N15/00,C12N5/00
            CC   97 human secreted proteins.
            FH   Key             Location/Qualifiers
            FT   source          1. .1447
            FT                   /organism='Homo sapiens (human)'.
FEATURES            Location/Qualifiers
     source         1. .1447
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
ORIGIN

  Query Match             98.4%;  Score 1324.6;  DB 6;  Length 1447;
  Best Local Similarity   99.3%;  Pred. No. 5e-262;
  Matches 1338;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAAA 1417


RESULT 9
BD083420
LOCUS       BD083420                1401 bp    DNA     linear   PAT 27-AUG-2002
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DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD083420
VERSION     BD083420.1  GI:22629030
KEYWORDS    JP 2001523950-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1401)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2001523950-A 2 27-NOV-2001;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2001523950-A/2
            PD   27-NOV-2001
            PF   23-JAN-1998 JP 1998532177
            PR   24-JAN-1997 US    08/788789
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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ORIGIN

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Db         65 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 124

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        185 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 244

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        245 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 304

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 364

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        365 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTA 424

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 484

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        485 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 544

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        545 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 604

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        605 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 664

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        665 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 724

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Db        725 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 784

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        785 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 844

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        845 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 904

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db        905 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 964

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Db        965 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1024

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Db       1025 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1084

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Db       1085 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1144

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Db       1145 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1204

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1205 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1264

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1265 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1324

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Db       1325 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1384

Qy       1320 TAAAAAAAAAAAAAAAA 1336
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Db       1385 AAAAAAAAAAAAAAAAA 1401


RESULT 10
AX083392
LOCUS       AX083392                1347 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 84 from Patent WO0112660.
ACCESSION   AX083392
VERSION     AX083392.1  GI:13185232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 84 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                     LTPL"
ORIGIN

  Query Match           97.3%;  Score 1309.4;  DB 6;  Length 1347;
  Best Local Similarity 99.8%;  Pred. No. 6.8e-259;
  Matches 1321;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db         20 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 79

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        140 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 199

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        320 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 379

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Db        440 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 499

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        500 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 559

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
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Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Db       1220 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1279

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Qy       1320 TAA 1322
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Db       1340 TGA 1342


RESULT 11
AF229179
LOCUS       AF229179                1345 bp    mRNA    linear   PRI 05-APR-2002
DEFINITION  Homo sapiens collectrin mRNA, complete cds.
ACCESSION   AF229179
VERSION     AF229179.1  GI:9957753
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K.,
            Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.
  TITLE     Collectrin, a collecting duct-specific transmembrane glycoprotein,
            is a novel homolog of ACE2 and is developmentally regulated in
            embryonic kidneys
  JOURNAL   J. Biol. Chem. 276 (20), 17132-17139 (2001)
  MEDLINE   21264468
   PUBMED   11278314
REFERENCE   2  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Human kidney specific membrane protein (NX-17)
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-2000) Department of Medicine III, Okayama
            University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,
            Japan
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ORIGIN

  Query Match            97.2%;  Score 1307.8;  DB 9;  Length 1345;
  Best Local Similarity  99.8%;  Pred. No. 1.4e-258;
  Matches 1320;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db         18 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 77

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         78 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 137

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        318 GTTGAAGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 377

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        498 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 557

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Db        558 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 617

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Db        618 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 677

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Db        678 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 737

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Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1278 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1337

Qy       1320 TAA 1322
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Db       1338 TGA 1340


RESULT 12
BD135300
LOCUS       BD135300                1356 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  110 human secretory proteins.
ACCESSION   BD135300
VERSION     BD135300.1  GI:23230245
KEYWORDS    JP 2002508167-A/51.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1356)
  AUTHORS   Moore,P.A., Ruben,S.M., Carter,K.C., Shi,Y., Rosen,C.A.,
            Soppet,D.R., Caou,H., Wei,Y.F., Florence,K., Duan,R.D.,
            Florence,C., Greene,J.M., Feng,P., Ferrie,A.M., Yu,G.L., Janat,F.
            and Ni,J.
  TITLE     110 human secretory proteins
  JOURNAL   Patent: JP 2002508167-A 51 19-MAR-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508167-A/51
            PD   19-MAR-2002
            PF   17-DEC-1998 JP 2000539040
            PR   18-DEC-1997 US   60/070 923,18-DEC-1997 US   60/068 007 PR
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            18-DEC-1997 US   60/068 008,18-DEC-1997 US   60/068 054 PR
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PI   PAUL A MOORE,STEVEN M RUBEN,KENNETH C CARTER,YANGGU SHI,CRAIG
PI   A ROSEN,
PI   DANIEL R SOPPET,HARA CAOU,YING FEI WEI,KIMBERLY FLORENCE, PI
ROSANNE D DUAN,
PI   CHARLES FLORENCE,JOHN M GREENE,PING FENG,ANN M FERRIE,GUO  PI
 LIANG YU,
PI   FORD JANAT,JIAN NI
PC   C12N15/09,A61K38/00,A61K48/00,A61P9/00,A61P9/10,A61P15/00, PC
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PC   A61P25/28,
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PC   C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,C12N15/00, PC
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PC   C12N5/00
CC   n equals a,t,g,or c
FH   Key             Location/Qualifiers
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FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1333;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    2;

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Db         12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 790

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        791 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 850

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 910

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Db        911 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 970

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Db        971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AGTGGAGGATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1090

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Db       1091 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1150

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCCAAAAA 1330

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1345
              ||||||||||||||||||||||||||
Db       1331 AAAAAAAAAAAAAAAAAAAAAAAAAA 1356

Search completed: June  6, 2004, 13:05:18
Job time : 5280.77 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 07:26:44 ; Search time 544.777 Seconds
(without alignments)
10496.171 Million cell updates/sec

Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgttgtggctgct.....aaaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 220

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1346	100.0	1346	3	AAZ65097	Aaz65097 Membrane-
2	1346	100.0	1346	3	AAC58612	Aac58612 Human PRO
3	1346	100.0	1346	3	AAA77680	Aaa77680 Human PRO
4	1346	100.0	1346	4	AAS21484	Aas21484 Human cDN
5	1346	100.0	1346	5	AAF44243	Aaf44243 Human PRO
6	1346	100.0	1346	7	ABX77959	Abx77959 Human PRO
7	1346	100.0	1346	7	ABX80371	Abx80371 Novel hum
8	1346	100.0	1346	7	ACA69277	Aca69277 Human cDN
9	1346	100.0	1346	7	ACD24093	Acd24093 Novel hum
10	1346	100.0	1346	7	ABX90348	Abx90348 Human sec
11	1346	100.0	1346	7	ABX64194	Abx64194 cDNA enco
12	1346	100.0	1346	7	ACA67234	Aca67234 cDNA enco
13	1346	100.0	1346	7	ACA64416	Aca64416 Novel hum
14	1346	100.0	1346	7	ACA03843	Aca03843 cDNA enco
15	1346	100.0	1346	7	ABX89381	Abx89381 DNA encod
16	1346	100.0	1346	7	ABX80875	Abx80875 Human sec
17	1346	100.0	1346	7	ACD44384	Acd44384 cDNA enco
18	1346	100.0	1346	7	ACD42035	Acd42035 Human sec
19	1346	100.0	1346	7	ABX79555	Abx79555 Human sec
20	1346	100.0	1346	7	ACA93576	Aca93576 Novel hum
21	1346	100.0	1346	7	ABX81258	Abx81258 Novel hum
22	1346	100.0	1346	7	ACA04264	Aca04264 Human cDN
23	1346	100.0	1346	7	ACA93074	Aca93074 Novel hum
24	1346	100.0	1346	7	ABX17158	Abx17158 Human PRO
25	1346	100.0	1346	8	ACA68013	Aca68013 Novel hum
26	1346	100.0	1346	8	ACA88462	Aca88462 Human sec
27	1346	100.0	1346	8	ACD81969	Acd81969 cDNA enco
28	1346	100.0	1346	8	ADA46000	Ada46000 Novel hum
29	1346	100.0	1346	8	ADA76431	Ada76431 Human PRO
30	1346	100.0	1346	8	ADA19081	Ada19081 Human PRO
31	1346	100.0	1346	8	ADA61704	Ada61704 Homo sapi
32	1346	100.0	1346	8	ADB19489	Adb19489 Novel hum
33	1346	100.0	1346	8	ADB28030	Adb28030 cDNA enco
34	1346	100.0	1346	8	ADA86509	Ada86509 Novel hum
35	1346	100.0	1346	8	ADB16073	Adb16073 Human PRO
36	1346	100.0	1346	8	ADA37897	Ada37897 Human cDN
37	1346	100.0	1346	8	ADA47859	Ada47859 Human PRO
38	1346	100.0	1346	8	ADA21583	Ada21583 Human cDN
39	1346	100.0	1346	8	ADA10370	Ada10370 Human cDN
40	1346	100.0	1346	8	ADA67654	Ada67654 Human PRO
41	1346	100.0	1346	8	ADB30661	Adb30661 cDNA enco
42	1346	100.0	1346	8	ADA85957	Ada85957 Novel hum
43	1346	100.0	1346	8	ADA17914	Ada17914 cDNA enco
44	1346	100.0	1346	8	ADA97169	Ada97169 Human PRO
45	1346	100.0	1346	8	ADA79473	Ada79473 Human PRO
46	1346	100.0	1346	8	ADA87612	Ada87612 Novel hum
47	1346	100.0	1346	8	ADB16814	Adb16814 Human PRO
48	1346	100.0	1346	8	ADA28022	Ada28022 Human cDN
49	1346	100.0	1346	8	ADA91906	Ada91906 Novel hum
50	1346	100.0	1346	8	ADB14969	Adb14969 Human PRO
51	1346	100.0	1346	8	ADB18930	Adb18930 Novel hum
52	1346	100.0	1346	8	ADA94145	Ada94145 Human PRO
53	1346	100.0	1346	8	ADB20041	Adb20041 Novel hum
54	1346	100.0	1346	8	ADB13353	Adb13353 Human PRO
55	1346	100.0	1346	8	ACD98664	Acd98664 Novel hum
56	1346	100.0	1346	8	ADA94602	Ada94602 Human cDN
57	1346	100.0	1346	8	ADA74607	Ada74607 Human PRO
58	1346	100.0	1346	8	ADB24840	Adb24840 Human PRO
59	1346	100.0	1346	8	ADA82364	Ada82364 Human PRO
60	1346	100.0	1346	8	ADA75327	Ada75327 Human PRO
61	1346	100.0	1346	8	ADA85405	Ada85405 Novel hum
62	1346	100.0	1346	8	ADA84853	Ada84853 Novel hum
63	1346	100.0	1346	8	ADB30109	Adb30109 cDNA enco
64	1346	100.0	1346	8	ADA80637	Ada80637 Human PRO
65	1346	100.0	1346	8	ADA75879	Ada75879 Human PRO
66	1346	100.0	1346	8	ADA38827	Ada38827 Human cDN
67	1346	100.0	1346	8	ADA47104	Ada47104 Human PRO
68	1346	100.0	1346	8	ADB25400	Adb25400 Human PRO
69	1346	100.0	1346	8	ADA93576	Ada93576 Human PRO
70	1346	100.0	1346	8	ADB26926	Adb26926 cDNA enco
71	1346	100.0	1346	8	ADB31213	Adb31213 cDNA enco
72	1346	100.0	1346	8	ADA92948	Ada92948 Human cDN
73	1346	100.0	1346	8	ADA61141	Ada61141 Homo sapi
74	1346	100.0	1346	8	ADB24288	Adb24288 Human PRO
75	1346	100.0	1346	8	ADA96617	Ada96617 Human PRO
76	1346	100.0	1346	8	ADA81189	Ada81189 Human PRO
77	1346	100.0	1346	8	ADA96065	Ada96065 Human PRO
78	1346	100.0	1346	8	ADB26374	Adb26374 cDNA enco
79	1346	100.0	1346	8	ADB21859	Adb21859 Novel hum
80	1346	100.0	1346	8	ADA77638	Ada77638 Human PRO
81	1346	100.0	1346	8	ADB18378	Adb18378 cDNA enco
82	1346	100.0	1346	8	ADA87061	Ada87061 Novel hum
83	1346	100.0	1346	8	ADA88164	Ada88164 Novel hum
84	1346	100.0	1346	8	ADA46552	Ada46552 Novel hum
85	1346	100.0	1346	8	ADB28582	Adb28582 cDNA enco
86	1346	100.0	1346	8	ADB29134	Adb29134 cDNA enco
87	1346	100.0	1346	8	ACH65530	Ach65530 Human cDN
88	1346	100.0	1346	8	ADA77086	Ada77086 Human PRO
89	1346	100.0	1346	8	ADA22509	Ada22509 Human cDN
90	1346	100.0	1346	8	ADA88716	Ada88716 Novel hum
91	1346	100.0	1346	8	ADA97721	Ada97721 Human PRO
92	1346	100.0	1346	8	ADB27478	Adb27478 cDNA enco
93	1346	100.0	1346	8	ADB22411	Adb22411 Novel hum
94	1346	100.0	1346	8	ACD39520	Acd39520 Human cDN
95	1346	100.0	1346	8	ADA06675	Ada06675 Human sec
96	1346	100.0	1346	8	ADA39368	Ada39368 Human cDN

97	1346	100.0	1346	8	ADA67102	Ada67102	Human PRO
98	1346	100.0	1346	8	ADB22963	Adb22963	Human PRO
99	1346	100.0	1346	8	ADB23736	Adb23736	Human PRO
100	1346	100.0	1346	8	ADA92458	Ada92458	Novel hum
101	1346	100.0	1346	8	ADB15521	Adb15521	Human PRO
102	1346	100.0	1346	8	ADB38773	Adb38773	Novel hum
103	1346	100.0	1346	8	ADB96394	Adb96394	Human PRO
104	1346	100.0	1346	8	ADB38221	Adb38221	Novel hum
105	1346	100.0	1346	9	ADB66693	Adb66693	Novel hum
106	1346	100.0	1346	9	ADB89773	Adb89773	Human PRO
107	1346	100.0	1346	9	ADB90505	Adb90505	Human PRO
108	1346	100.0	1346	9	ADB39606	Adb39606	Novel hum
109	1346	100.0	1346	9	ADB47229	Adb47229	Novel hum
110	1346	100.0	1346	9	ADB86836	Adb86836	Human PRO
111	1346	100.0	1346	9	ADB77441	Adb77441	Novel hum
112	1346	100.0	1346	9	ADB34598	Adb34598	Human PRO
113	1346	100.0	1346	9	ADB35702	Adb35702	Human PRO
114	1346	100.0	1346	9	ADB34046	Adb34046	Human PRO
115	1346	100.0	1346	9	ADB35150	Adb35150	Human PRO
116	1346	100.0	1346	9	ADB36254	Adb36254	Human PRO
117	1346	100.0	1346	9	ADB46649	Adb46649	Novel hum
118	1346	100.0	1346	9	ADC57866	Adc57866	Human PRO
119	1346	100.0	1346	9	ADC55230	Adc55230	Human PRO
120	1346	100.0	1346	9	ADC12097	Adc12097	Human cDN
121	1346	100.0	1346	9	ADC56519	Adc56519	Human PRO
122	1346	100.0	1346	9	ADC07574	Adc07574	Human cDN
123	1346	100.0	1346	9	ADC11564	Adc11564	Human cDN
124	1346	100.0	1346	9	ADC50522	Adc50522	Novel hum
125	1346	100.0	1346	9	ADC72069	Adc72069	Novel hum
126	1346	100.0	1346	9	ADC60048	Adc60048	Novel hum
127	1346	100.0	1346	9	ADC53055	Adc53055	Novel hum
128	1346	100.0	1346	9	ADC57409	Adc57409	Novel hum
129	1346	100.0	1346	9	ADC60600	Adc60600	Novel hum
130	1346	100.0	1346	9	ADC51075	Adc51075	Novel hum
131	1346	100.0	1346	9	ADC65602	Adc65602	Human PRO
132	1346	100.0	1346	9	ADC54700	Adc54700	Novel hum
133	1346	100.0	1346	9	ADC53661	Adc53661	Novel hum
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138	1346	100.0	1346	9	ADD08218	Add08218	Novel hum
139	1346	100.0	1346	9	ADD03306	Add03306	Novel hum
140	1346	100.0	1346	9	ADC90298	Adc90298	Novel hum
141	1346	100.0	1346	9	ADC82043	Adc82043	Human PRO
142	1346	100.0	1346	9	ADC69717	Adc69717	cDNA enco
143	1346	100.0	1346	9	ADC48606	Adc48606	Human PRO
144	1346	100.0	1346	9	ADD10135	Add10135	Human PRO
145	1346	100.0	1346	9	ADD07685	Add07685	Novel hum
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147	1346	100.0	1346	9	ADC82576	Adc82576	Human PRO
148	1346	100.0	1346	9	ADC80666	Adc80666	Novel hum
149	1346	100.0	1346	9	ADD11173	Add11173	Human PRO
150	1346	100.0	1346	9	ADC48054	Adc48054	Human PRO
151	1346	100.0	1346	9	ADD08756	Add08756	Novel hum
152	1346	100.0	1346	9	ADC80114	Adc80114	Novel hum
153	1346	100.0	1346	9	ADD07005	Add07005	Novel hum
154	1346	100.0	1346	9	ADD09583	Add09583	Human PRO
155	1346	100.0	1346	9	ADC83252	Adc83252	Human PRO
156	1346	100.0	1346	9	ADD41296	Add41296	Novel hum
157	1346	100.0	1346	9	ADD52435	Add52435	cDNA enco
158	1346	100.0	1346	9	ADD53175	Add53175	cDNA enco
159	1346	100.0	1346	9	ADD53727	Add53727	Novel hum
160	1346	100.0	1346	9	ADD55359	Add55359	Human PRO
161	1346	100.0	1346	9	ADD56317	Add56317	Human PRO
162	1346	100.0	1346	9	ADD51883	Add51883	cDNA enco
163	1346	100.0	1346	9	ADD02682	Add02682	Human PRO
164	1346	100.0	1346	9	ADD02116	Add02116	Human PRO
165	1346	100.0	1346	9	ADD54298	Add54298	Novel hum
166	1346	100.0	1346	9	ADD54755	Add54755	Human PRO
167	1346	100.0	1346	9	ADD92615	Add92615	Human PRO
168	1346	100.0	1346	9	ADD91511	Add91511	Human PRO
169	1346	100.0	1346	9	ADE04125	Ade04125	Human PRO
170	1346	100.0	1346	9	ADE26909	Ade26909	Novel hum
171	1346	100.0	1346	9	ADE32422	Ade32422	Novel hum
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173	1346	100.0	1346	9	ADD79578	Add79578	cDNA enco
174	1346	100.0	1346	9	ADE42114	Ade42114	Human PRO
175	1346	100.0	1346	9	ADE17931	Ade17931	Human PRO
176	1346	100.0	1346	9	ADD92063	Add92063	Human PRO
177	1346	100.0	1346	9	ADE33526	Ade33526	Novel hum
178	1346	100.0	1346	9	ADE34078	Ade34078	Novel hum
179	1346	100.0	1346	9	ADD80130	Add80130	cDNA enco
180	1346	100.0	1346	9	ADD93167	Add93167	Human PRO
181	1346	100.0	1346	9	ADE19587	Ade19587	Human PRO
182	1346	100.0	1346	9	ADE19035	Ade19035	Human PRO
183	1346	100.0	1346	9	ADE43231	Ade43231	Human PRO
184	1346	100.0	1346	9	ADD96020	Add96020	Human PRO
185	1346	100.0	1346	9	ADE22906	Ade22906	cDNA enco
186	1346	100.0	1346	9	ADD79024	Add79024	cDNA enco
187	1346	100.0	1346	9	ADE26376	Ade26376	Novel hum
188	1346	100.0	1346	9	ADE32974	Ade32974	Novel hum
189	1346	100.0	1346	9	ADE42666	Ade42666	Human PRO
190	1346	100.0	1346	9	ADD80682	Add80682	cDNA enco
191	1346	100.0	1346	9	ADD89710	Add89710	Human PRO
192	1346	100.0	1346	9	ADE40994	Ade40994	Human PRO
193	1346	100.0	1346	9	ADE04793	Ade04793	Human PRO
194	1346	100.0	1346	10	ADC81218	Adc81218	Novel hum
195	1346	100.0	1346	10	ADD76666	Add76666	Human PRO
196	1346	100.0	1346	10	ADD88030	Add88030	Human PRO
197	1346	100.0	1346	10	ADD86434	Add86434	Human PRO
198	1346	100.0	1346	10	ADE75882	Ade75882	Human PRO
199	1346	100.0	1346	10	ADE23458	Ade23458	cDNA enco
200	1346	100.0	1346	10	ADE24010	Ade24010	cDNA enco
201	1346	100.0	1346	10	ADE24653	Ade24653	cDNA enco
202	1346	100.0	1346	10	ADD87478	Add87478	Human PRO
203	1346	100.0	1346	10	ADE89344	Ade89344	Human PRO
204	1346	100.0	1346	10	ADE18483	Ade18483	Human PRO
205	1346	100.0	1346	10	ADE88792	Ade88792	Human PRO
206	1325.4	98.5	1432	7	ADA56090	Ada56090	Gene enco
207	1325.4	98.5	1432	7	ADA39900	Ada39900	Human sec
208	1325.4	98.5	1432	8	ADA11489	Ada11489	Human cDN
209	1325.4	98.5	1432	9	ADD37613	Add37613	Human sec
210	1324.6	98.4	1447	3	AAZ65261	Aaz65261	Human sec
211	1324.6	98.4	1447	9	ADE11650	Ade11650	Human sec
212	1321.8	98.2	1401	2	AAV40540	Aav40540	Homo sapi
213	1309.4	97.3	1347	4	AAF94470	Aaf94470	Human hyd
214	1307.8	97.2	1345	7	ABZ78127	Abz78127	Human can
c 215	1307.4	97.1	1365	4	AAH98224	Aah98224	Human EST
216	1305	97.0	1356	2	AAX97957	Aax97957	Human sec
217	1305	97.0	1356	7	ADA56545	Ada56545	Gene enco
218	1305	97.0	1356	7	ADA40381	Ada40381	Human sec
219	1305	97.0	1356	8	ADA11594	Ada11594	Human cDN
220	1305	97.0	1356	9	ADD37752	Add37752	Human sec

ALIGNMENTS

RESULT 1
AAZ65097
ID AAZ65097 standard; cDNA; 1346 BP.
XX
AC AAZ65097;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1312 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX

```
Db        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080

Qy       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140

Qy       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAA 1346
              |||||||||||||||||||||||||
Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAA 1346


RESULT 203
ADE89344
ID   ADE89344 standard; cDNA; 1346 BP.
XX
AC   ADE89344;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human PRO polynucleotide #241.
XX
KW   Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW   cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW   liver; microvascular endothelial cell; glucose; FFA;
KW   skeletal muscle cell; adipocyte cell; pericyte cell;
KW   inner ear utricular supporting cell; T-lymphocyte cell;
KW   endothelial cell tube formation; bone disorder; cartilage disorder;
KW   sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW   rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW   immune system cell infiltration.
XX
OS   Homo sapiens.
XX
PN   US2003199062-A1.
XX
PD   23-OCT-2003.
XX
PF   17-APR-2002; 2002US-00124823.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   10-MAR-1999; 2000WO-US006319.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   22-DEC-1999;   99WO-US030720.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005841.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   18-MAY-2001; 2001US-00860216.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
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PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2004-041360/04.
DR P-PSDB; ADE89345.
XX
PT Novel isolated PRO polypeptide useful for treating diabetes, hyper- or
PT hypo-insulinemia, sports injuries, arthritis, obesity, stroke, heart
PT attack, various coagulation disorders, tumors.
XX
PS Claim 2; SEQ ID NO 481; 638pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600

Qy        601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660
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Db        601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660

Qy        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720

Qy        721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780

Qy        781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840
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Db        781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840

Qy        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900

Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
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Db       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080

Qy       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
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Qy       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
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Db       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
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Db       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
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Db       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
             ||||||||||||||||||||||||||
Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 204
ADE18483
ID ADE18483 standard; cDNA; 1346 BP.
XX
AC ADE18483;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PRO polynucleotide #241.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.
XX
OS Homo sapiens.
XX
PN US2003194794-A1.
XX
PD 16-OCT-2003.
XX
PF 17-APR-2002; 2002US-00125805.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
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PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 10-MAR-1999; 2000WO-US006319.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
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PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX

PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2004-021079/02.
DR P-PSDB; ADE18484.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, for use in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; SEQ ID NO 481; 638pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy   61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180

Qy  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

Qy  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300

Qy  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420

Qy  421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Qy  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540

Qy  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600

Qy  601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660
Db  601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660

Qy  661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720
Db  661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720

Qy  721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780
Db  721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780

Qy  781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840
Db  781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840

Qy  841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900
Db  841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900

Qy  901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
Db  901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy  961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
Db  961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy 1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
Db 1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080

Qy 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
Db 1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140

Qy 1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
Db 1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy 1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
Db 1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy 1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
Db 1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 205
ADE88792
ID ADE88792 standard; cDNA; 1346 BP.
XX
AC ADE88792;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PRO polynucleotide #241.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.
XX
OS Homo sapiens.
XX
PN US2003199054-A1.
XX
PD 23-OCT-2003.
XX
PF 12-APR-2002; 2002US-00121054.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 10-MAR-1999; 2000WO-US006319.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2004-041356/04.
DR P-PSDB; ADE88793.
XX
PT Novel secreted and transmembrane polypeptides, PRO useful for treating
PT bone disorders, arthritis, heart attack, injuries, tumors, and
PT stimulating release of TNF-alpha from human blood.
XX
PS Claim 2; SEQ ID NO 481; 638pp; English.
XX

CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Db        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540

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Db        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600

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Db        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720

Qy        721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780
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Qy        781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840

Qy        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900

Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
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Db        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
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Db        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
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Qy       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
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Db       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140

Qy       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              ||||||||||||||||||||||||||
Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 206
ADA56090
ID ADA56090 standard; DNA; 1432 BP.
XX
AC ADA56090;
XX
DT 20-NOV-2003 (first entry)
XX
DE Gene encoding human secreted protein #269.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;

KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR P-PSDB; ADA56986.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 21; SEQ ID NO 279; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.5%; Score 1325.4; DB 7; Length 1432;
Best Local Similarity 99.5%; Pred. No. 2.4e-258;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 122

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 182

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 242

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 302

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 362

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 422

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 482

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 542

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 602

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 662

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        663 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 722

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 782

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 842

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 902

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 962

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1022

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1082

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1142

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1202
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Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1262

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1322

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1382

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
             || |  ||||||||||||||||||||||
Db       1383 TGATTGTGAAAAAAAAAAAAAAAAAA 1409
```

RESULT 207
ADA39900
ID ADA39900 standard; cDNA; 1432 BP.
XX
AC ADA39900;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOMB SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 9; SEQ ID NO 282; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.5%; Score 1325.4; DB 7; Length 1432;
Best Local Similarity 99.5%; Pred. No. 2.4e-258;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 122

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 182

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 242

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 302

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 362

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 422

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        423 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 482

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        483 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 542

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 602

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 662

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        663 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 722

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 782

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 842
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Qy       780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
Db       843 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 902

Qy       840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
Db       903 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 962

Qy       900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
Db       963 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1022

Qy       960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
Db      1023 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1082

Qy      1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
Db      1083 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1142

Qy      1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
Db      1143 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1202

Qy      1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
Db      1203 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1262

Qy      1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
Db      1263 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1322

Qy      1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
Db      1323 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1382

Qy      1320 TAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db      1383 TGATTGTGAAAAAAAAAAAAAAAAAAAA 1409
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RESULT 208
ADA11489
ID ADA11489 standard; DNA; 1432 BP.
XX
AC ADA11489;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
XX
KW cancer; inflammation; immune disorder; neurological disorder;
KW blood clotting disorder; food additive; food preservative;
KW storage capability; fat content; nutritional component; ds; gene; human.
XX
OS Homo sapiens.
XX
PN US2003055236-A1.
XX
PD 20-MAR-2003.
XX
PF 14-MAR-2002; 2002US-00097065.
XX
PR 18-DEC-1997; 97US-0068006P.
PR 18-DEC-1997; 97US-0068007P.
PR 18-DEC-1997; 97US-0068008P.
PR 18-DEC-1997; 97US-0068053P.
PR 18-DEC-1997; 97US-0068054P.
PR 18-DEC-1997; 97US-0068057P.
PR 18-DEC-1997; 97US-0068064P.
PR 18-DEC-1997; 97US-0070923P.
PR 19-DEC-1997; 97US-0068169P.
PR 19-DEC-1997; 97US-0068365P.
PR 19-DEC-1997; 97US-0068367P.
PR 19-DEC-1997; 97US-0068368P.
PR 19-DEC-1997; 97US-0068369P.
PR 17-DEC-1998; 98WO-US027059.
PR 17-JUN-1999; 99US-00334595.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence KA, Duan DR, Florence C, Greene JM, Feng P;
PI Ferrie AM, Yu G, Janat F, Ni J;
XX
DR WPI; 2003-567105/53.
DR P-PSDB; ADA11613.
XX
PT New secreted HKABT24 nucleic acid molecules and polypeptides, useful for
PT preventing, treating, or ameliorating a medical condition, such as
PT cancer, inflammation, immune disorders, neurological and blood clotting
PT disorders.
XX
PS Claim 1; SEQ ID NO 17; 118pp; English.
XX
CC The invention relates to an isolated HKABT24 nucleic acid molecule. The
CC polypeptides, nucleic acids and antibodies are useful for diagnosing a
CC pathological condition or a susceptibility to a pathological condition,
CC for preventing, treating, or ameliorating a medical condition, such as
CC cancer, inflammation and other immune disorders, neurological and blood
CC clotting disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
CC antagonist may also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content or other
CC nutritional components. The present sequence represents cDNA encoding a
CC novel human secreted protein. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
XX
SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.5%; Score 1325.4; DB 8; Length 1432;
Best Local Similarity 99.5%; Pred. No. 2.4e-258;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```
Qy         1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db        63 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 122

Qy        61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db       123 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 182

Qy       121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db       183 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 242

Qy       181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db       243 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 302

Qy       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db       303 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 362

Qy       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db       363 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 422

Qy       361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db       423 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 482
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Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 542

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 602

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 662

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        663 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 722

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 782

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 842

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 902

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 962

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1022

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1082

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1142

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1202

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1262

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1322

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1382

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |    ||||||||||||||||||||
Db       1383 TGATTGTGAAAAAAAAAAAAAAAAAAAA 1409
```

RESULT 209
ADD37613
ID ADD37613 standard; cDNA; 1432 BP.
XX
AC ADD37613;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted protein encoding sequence #95.
XX
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US008279.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-140218/13.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or asthmatic disorders, or related immediate
PT hypersensitivity disorders.
XX
PS Claim 7; SEQ ID NO 95; 1323pp; English.
XX
CC The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or asthmatic disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases , wound healing and disorders of epithelial cell
CC proliferation, immune disorders , cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders , or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein encoding sequence.
XX
SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.5%; Score 1325.4; DB 9; Length 1432;
Best Local Similarity 99.5%; Pred. No. 2.4e-258;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 122

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 182

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 242

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 302
```

```
Qy       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       303 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 362

Qy       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       363 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 422

Qy       361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       423 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 482

Qy       421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       483 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 542

Qy       481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       543 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 602

Qy       541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       603 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 662

Qy       601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       663 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 722

Qy       660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       723 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 782

Qy       720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       783 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 842

Qy       780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       843 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 902

Qy       840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       903 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 962

Qy       900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       963 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1022

Qy       960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1023 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1082

Qy      1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1083 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1142

Qy      1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1143 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1202

Qy      1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1203 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1262

Qy      1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1263 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1322

Qy      1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1323 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1382

Qy      1320 TAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
             | |    ||||||||||||||||||||
Db      1383 TGATTGTGAAAAAAAAAAAAAAAAAAA 1409
```

RESULT 210
AAZ65261
ID AAZ65261 standard; DNA; 1447 BP.
XX
AC AAZ65261;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human secreted protein gene 12.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9958660-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009847.
XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R;
XX
DR WPI; 2000-062296/05.
DR P-PSDB; AAY76135.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 303; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 97 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,

```
CC   atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC   digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC   also useful for identifying their binding partners. The sequences shown
CC   in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ   Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

  Query Match             98.4%;  Score 1324.6;  DB 3;  Length 1447;
  Best Local Similarity   99.3%;  Pred. No. 3.5e-258;
  Matches 1338;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              |||     ||||||||||||||||||||
Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAA 1417


RESULT 211
ADE11650
ID   ADE11650 standard; cDNA; 1447 BP.
XX
AC   ADE11650;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human secreted polypeptide cDNA #12.
XX
KW   Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
KW   Alzheimer's disease; human; ss; gene.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003100051-A1.
XX
PD   29-MAY-2003.
XX
PF   10-SEP-2001; 2001US-00948783.
XX
PR   12-MAY-1998;   98US-0085093P.
PR   12-MAY-1998;   98US-0085094P.
PR   12-MAY-1998;   98US-0085105P.
PR   12-MAY-1998;   98US-0085180P.
PR   18-MAY-1998;   98US-0085906P.
PR   18-MAY-1998;   98US-0085920P.
PR   18-MAY-1998;   98US-0085921P.
PR   18-MAY-1998;   98US-0085922P.
PR   18-MAY-1998;   98US-0085923P.
PR   18-MAY-1998;   98US-0085924P.
PR   18-MAY-1998;   98US-0085925P.
PR   18-MAY-1998;   98US-0085927P.
PR   18-MAY-1998;   98US-0085928P.
PR   06-MAY-1999;   99WO-US009847.
PR   10-NOV-1999;   99US-00437658.
PR   11-SEP-2000; 2000US-0231846P.
PR   28-JUN-2001; 2001US-00892877.
XX
PA   (RUBE/) RUBEN S M.
PA   (FLOR/) FLORENCE K A.
```

PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
XX
PI Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R, Birse CE;
XX
DR WPI; 2003-801210/75.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX
PS Claim 1; SEQ ID NO 22; 453pp; English.
XX
CC The invention relates to human secreted polypeptides and the
CC polynucleotides encoding them. The sequences are useful for preparing
CC medicaments for preventing, treating or ameliorating medical conditions
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC as Alzheimer's disease. This sequence represents cDNA encoding a human
CC secreted polypeptide of the invention.
XX
SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.4%; Score 1324.6; DB 9; Length 1447;
Best Local Similarity 99.3%; Pred. No. 3.5e-258;
Matches 1338; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

```
Qy    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db   71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy   61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db  131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db  191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db  251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db  311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db  371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db  431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy  421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db  491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db  551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db  611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy  601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
Db  671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy  660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
Db  731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy  720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
Db  791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy  780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
Db  851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy  840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
Db  911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy  900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
Db  971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy  960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
Db 1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy 1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
Db 1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy 1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
Db 1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy 1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
Db 1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy 1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
Db 1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy 1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
Db 1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy 1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db 1391 TGATTGTGAAAAAAAAAAAAAAAAAA 1417
```

RESULT 212
AAV40540
ID AAV40540 standard; cDNA; 1401 BP.
XX
AC AAV40540;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens secreted protein clone AM42_3.
XX
KW Clone; secreted protein; ds.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
FT   CDS             71. .739
FT                   /*tag= a
FT                   /note= "secreted protein"
XX
PN   WO9832853-A2.
XX
PD   30-JUL-1998.
XX
PF   23-JAN-1998;   98WO-US001396.
XX
PR   24-JAN-1997;   97US-00788789.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI   Spaulding V, Agostino MJ;
XX
DR   WPI; 1998-427949/36.
DR   P-PSDB; AAW29670.
XX
PT   New isolated polynucleotide(s) and secreted proteins - isolated from
PT   human foetal kidney, adult brain, adult salivary gland, foetal brain and
PT   adult testes cDNA libraries.
XX
PS   Claim 16; Page 64-65; 109pp; English.
XX
CC   The sequence is that of encoding a secreted protein. Such a protein can
CC   have biological activities, e.g. nutritional activity, cytokine and cell
CC   proliferation/differentiation activity, immune stimulating or suppressing
CC   activity, haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity, and other activities
XX
SQ   Sequence 1401 BP; 458 A; 258 C; 251 G; 434 T; 0 U; 0 Other;

  Query Match             98.2%;  Score 1321.8;  DB 2;  Length 1401;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-257;
  Matches 1334;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 124

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 184

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 244

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 304

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 364

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        365 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTA 424

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 484

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        485 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 544

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 604

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 664

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        665 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 724

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 784

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 844

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 904

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 964

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1024

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1084

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1144

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1204

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1264

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1324

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1384

Qy       1320 TAAAAAAAAAAAAAAAA 1336
              |||||||||||||||||
Db       1385 AAAAAAAAAAAAAAAAA 1401


RESULT 213
AAF94470
ID   AAF94470 standard; cDNA; 1347 BP.
XX
AC   AAF94470;
XX
DT   04-JUN-2001  (first entry)
XX
DE   Human hydrophobic domain containing protein clone HP10720 cDNA #84.
XX
```

KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW behavioural characteristic; immune response; ss.
XX
OS Homo sapiens.
XX
PN WO200112660-A2.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000WO-JP005356.
XX
PR 17-AUG-1999; 99JP-00230344.
PR 07-SEP-1999; 99JP-00252551.
PR 01-OCT-1999; 99JP-00281132.
PR 22-OCT-1999; 99JP-00301624.
PR 04-NOV-1999; 99JP-00313877.
XX
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-160059/16.
DR P-PSDB; AAB88580.
XX
PT Human proteins with hydrophobic domains and the DNAs which encode them
PT are useful for treating autoimmune disorders, burns and tumors and for
PT screening novel pharmaceuticals.
XX
PS Claim 4; Page 384-386; 518pp; English.
XX
CC AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC for genetic diagnosis and gene sources for gene therapy or for producing
CC (I) in large quantities. Cells containing (II) are used for the detection
CC of ligands or receptors corresponding to membrane or secretory proteins
CC and to screen small molecule novel pharmaceuticals. Antibodies directed
CC to (I) can be used for the detection, quantification and purification of
CC (I). Activities of (I) may include cytokine and cell
CC proliferation/differentiation function, immune stimulating or suppressing
CC activity, haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC inflammatory bowel disease and tumours. (I) and (II) can also be used for
CC wound healing, as nutritional sources or supplements e.g. as amino acid,
CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC processing and utilisation of dietary fat, protein, carbohydrate,
CC vitamins and minerals, to effect behavioural characteristics, to affect
CC appetite, and can act as antigens in vaccines to raise an immune response
CC to the protein or another material cross-reactive with the protein
XX
SQ Sequence 1347 BP; 434 A; 252 C; 243 G; 418 T; 0 U; 0 Other;

Query Match 97.3%; Score 1309.4; DB 4; Length 1347;
Best Local Similarity 99.8%; Pred. No. 4e-255;
Matches 1321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 79

Qy   61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 139

Qy  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  140 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 199

Qy  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  200 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 259

Qy  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  260 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 319

Qy  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  320 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 379

Qy  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  380 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 439

Qy  421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  440 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 499

Qy  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  500 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 559

Qy  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  560 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 619

Qy  601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  620 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 679

Qy  660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  680 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 739

Qy  720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  740 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 799

Qy  780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  800 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 859

Qy  840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  860 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 919

Qy  900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  920 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 979

Qy  960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  980 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1039

Qy 1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1040 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1099

Qy 1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1100 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1159

Qy 1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1160 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1219
```

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Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1220 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1279

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1280 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1339

Qy       1320 TAA 1322
              | |
Db       1340 TGA 1342
```

RESULT 214
ABZ78127
ID ABZ78127 standard; cDNA; 1345 BP.
XX
AC ABZ78127;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related coding sequence, 156P1D4.
XX
KW Human; cytostatic; vaccine; cancer; immune response; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
DR P-PSDB; ABR01796.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 26; Fig 2G; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. 74P3B3 maps
CC to chromosome 8p21.3-p22, 83P4B8 maps to chromosome 15q25.1, 109P1D4 maps
CC to chromosome Xq21.3, 151P1C7A maps to chromosome 10q11.2, 151P4E11 maps
CC to chromosome 11q13.3-q13.5, 154P2A8 maps to chromosome 3q24, 156P1D4
CC maps to chromosome Xp22.3, 156P5C12 maps to chromosome 2p13.1-p12,
CC 159P2B5 maps to chromosome 7p15.1, 161P2B7A maps to chromosome 3q25-q26,
CC 179P3G7 maps to chromosome 12q12-q13, 184P3C10B maps to chromosome
CC 19p13.1, 184P3G10 maps to chromosome 2p12, 185P2C9 maps to chromosome
CC 18p11.22, 185P3C2 maps to chromosome 17q21, 186P1H9 maps to chromosome
CC 7q21.3-q22.1, 187P3F2 maps to chromosome 3p14.2 and 192P2G7 maps to
CC chromosome 22q13.2-q13.31

XX
SQ Sequence 1345 BP; 435 A; 251 C; 241 G; 418 T; 0 U; 0 Other;

Query Match 97.2%; Score 1307.8; DB 7; Length 1345;
Best Local Similarity 99.8%; Pred. No. 8.5e-255;
Matches 1320; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 77

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 137

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 197

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 257

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 317

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 GTTGAAGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 377

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 437

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 497

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 557

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 617

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        618 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 677

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 737

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 797

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 857

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 917

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 977

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        978 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1037

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1097

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1157

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1217

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1277

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1337

Qy       1320 TAA 1322
              |||
Db       1338 TGA 1340


RESULT 215
AAH98224/c
ID   AAH98224 standard; cDNA; 1365 BP.
XX
AC   AAH98224;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Human EST-derived coding sequence SEQ ID NO: 81.
XX
KW   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW   gene therapy; nutrition; ss.
XX
OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002687.
XX
PR   25-JAN-2000; 2000US-00491404.
PR   17-JUL-2000; 2000US-00617746.
PR   03-AUG-2000; 2000US-00631451.
PR   15-SEP-2000; 2000US-00663870.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Qian XB,  Wang Z,  Chen R,  Asundi V;
PI   Cao Y,  Drmanac RA,  Zhang J,  Werhman T;
XX
DR   WPI; 2001-476164/51.
DR   P-PSDB; AAM23565.
XX
PT   Isolated polypeptide for treatment of diseases, diagnostics, raising
PT   antibodies and research use.
XX
PS   Claim 1; Page 234; 1275pp; English.
XX
CC   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a cDNA
CC   of the invention
XX
SQ   Sequence 1365 BP; 416 A; 244 C; 257 G; 448 T; 0 U; 0 Other;

  Query Match             97.1%;  Score 1307.4;  DB 4;  Length 1365;
  Best Local Similarity   99.4%;  Pred. No. 1e-254;
  Matches 1333;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    2;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1341 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 1282

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1281 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 1222

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1221 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 1162

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1161 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 1102

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1101 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 1042

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1041 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 982

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 922

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 862

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 802

Qy        541 GTGGATGACGCTGAAG-ATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTC 599
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        801 GTGGATGACGCTGAAGAATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTC 742

Qy        600 TGATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAG 658
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        741 TGATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAG 682

Qy        659 GCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCT 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCT 622

Qy        719 GTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTC 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 GTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTC 562

Qy        779 TTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCA 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCA 502

Qy        839 ACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 ACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAG 442

Qy        899 TATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAA 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAA 382
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Qy       959 TAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTC 1018
Db       381 TAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTC 322

Qy      1019 CAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTTGACGAT 1078
Db       321 CAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTTGACGAT 262

Qy      1079 CACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATG 1138
Db       261 CACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATG 202

Qy      1139 GATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAA 1198
Db       201 GATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAA 142

Qy      1199 CAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCA 1258
Db       141 CAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCA 82

Qy      1259 TTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTT 1318
Db         81 TTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTT 22

Qy      1319 TTAAAAAAAAAAAAAAAAAAA 1339
Db         21 TTGATTGTGAAAAAAAAAAAA 1
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RESULT 216
AAX97957
ID AAX97957 standard; DNA; 1356 BP.
XX
AC AAX97957;
XX
DT 17-SEP-1999 (first entry)
XX
DE Human secreted protein gene 42.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO9931117-A1.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-US027059.
XX
PR 18-DEC-1997; 97US-0068006P.
PR 18-DEC-1997; 97US-0068007P.
PR 18-DEC-1997; 97US-0068008P.
PR 18-DEC-1997; 97US-0068053P.
PR 18-DEC-1997; 97US-0068054P.
PR 18-DEC-1997; 97US-0068057P.
PR 18-DEC-1997; 97US-0068064P.
PR 18-DEC-1997; 97US-0070923P.
PR 19-DEC-1997; 97US-0068169P.
PR 19-DEC-1997; 97US-0068365P.
PR 19-DEC-1997; 97US-0068367P.
PR 19-DEC-1997; 97US-0068368P.
PR 19-DEC-1997; 97US-0068369P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence K, Duan RD, Florence C, Greene JM, Feng P;
PI Ferrie AM, Yu G, Janat F, Ni J;
XX
DR WPI; 1999-418749/35.
DR P-PSDB; AAY36265.
XX
PT New isolated human genes encoding secreted polypeptides.
XX
PS Claim 1; Page 296-297; 537pp; English.
XX
CC AAX97916 to AAX98029 represent 110 isolated human secreted protein genes.
CC AAY36224 to AAY36727 represent the secreted proteins encoded by the 110
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 110 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences given
CC in AAX97907 to AAX97915 and AAY36223 are used in the exemplification of
CC the present invention
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 97.0%; Score 1305; DB 2; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db         12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db         72 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 131

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db        132 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 191

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db        192 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 251

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db        252 CAGA-GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 310

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db        311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db        371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db        431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db        491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db        551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610
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Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 790

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 850

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 910

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 970

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AGTGGAGGATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1090

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1150

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              |||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCCAAAAA 1330

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1345
              |||||||||||||||||||||||||
Db       1331 AAAAAAAAAAAAAAAAAAAAAAAAAA 1356
```

RESULT 217
ADA56545
ID ADA56545 standard; DNA; 1356 BP.
XX
AC ADA56545;
XX
DT 20-NOV-2003 (first entry)
XX
DE Gene encoding human secreted protein #269.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR P-PSDB; ADA57438.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 21; SEQ ID NO 734; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 97.0%; Score 1305; DB 7; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 131

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        132 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 191
Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db        192 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 251
Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db        252 CAGA-GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 310
Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db        311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370
Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db        371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430
Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db        431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490
Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db        491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550
Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db        551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610
Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
Db        611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670
Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
Db        671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730
Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
Db        731 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 790
Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
Db        791 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 850
Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
Db        851 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 910
Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
Db        911 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 970
Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
Db        971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030
Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
Db       1031 AGTGGAGGATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1090
Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
Db       1091 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1150
Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
Db       1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210
Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
Db       1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270
Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
Db       1271 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCCAAAAA 1330
Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1345
Db       1331 AAAAAAAAAAAAAAAAAAAAAAAAAA 1356
```

RESULT 218
ADA40381
ID ADA40381 standard; cDNA; 1356 BP.
XX
AC ADA40381;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 9; SEQ ID NO 763; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also

CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 97.0%; Score 1305; DB 7; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

```
Qy    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy   61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 131

Qy  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  132 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 191

Qy  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  192 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 251

Qy  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252 CAGA-GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 310

Qy  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370

Qy  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430

Qy  421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490

Qy  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550

Qy  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610

Qy  601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670

Qy  660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730

Qy  720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  731 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 790

Qy  780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  791 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 850

Qy  840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  851 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 910

Qy  900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  911 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 970

Qy  960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030

Qy 1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1031 AGTGGAGGATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1090

Qy 1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1091 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1150

Qy 1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
          |||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||||
Db 1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210

Qy 1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270

Qy 1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1271 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCCAAAAA 1330

Qy 1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1345
          |||||||||||||||||||||||||
Db 1331 AAAAAAAAAAAAAAAAAAAAAAAAA 1356
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RESULT 219
ADA11594
ID ADA11594 standard; DNA; 1356 BP.
XX
AC ADA11594;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.
XX
KW cancer; inflammation; immune disorder; neurological disorder;
KW blood clotting disorder; food additive; food preservative;
KW storage capability; fat content; nutritional component; ds; gene; human.
XX
OS Homo sapiens.
XX
PN US2003055236-A1.
XX
PD 20-MAR-2003.
XX
PF 14-MAR-2002; 2002US-00097065.
XX
PR 18-DEC-1997; 97US-0068006P.
PR 18-DEC-1997; 97US-0068007P.
PR 18-DEC-1997; 97US-0068008P.
PR 18-DEC-1997; 97US-0068053P.
PR 18-DEC-1997; 97US-0068054P.
PR 18-DEC-1997; 97US-0068057P.
PR 18-DEC-1997; 97US-0068064P.
PR 18-DEC-1997; 97US-0070923P.
PR 19-DEC-1997; 97US-0068169P.
PR 19-DEC-1997; 97US-0068365P.
PR 19-DEC-1997; 97US-0068367P.
PR 19-DEC-1997; 97US-0068368P.
PR 19-DEC-1997; 97US-0068369P.
PR 17-DEC-1998; 98WO-US027059.
PR 17-JUN-1999; 99US-00334595.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence KA, Duan DR, Florence C, Greene JM, Peng P;
PI Ferrie AM, Yu G, Janat F, Ni J;
XX
DR WPI; 2003-567105/53.
DR P-PSDB; ADA11718.
XX
PT New secreted HKABT24 nucleic acid molecules and polypeptides, useful for
PT preventing, treating, or ameliorating a medical condition, such as
PT cancer, inflammation, immune disorders, neurological and blood clotting
PT disorders.
XX
PS Claim 1; SEQ ID NO 122; 118pp; English.
XX
CC The invention relates to an isolated HKABT24 nucleic acid molecule. The
CC polypeptides, nucleic acids and antibodies are useful for diagnosing a
CC pathological condition or a susceptibility to a pathological condition,
CC for preventing, treating, or ameliorating a medical condition, such as
CC cancer, inflammation and other immune disorders, neurological and blood
CC clotting disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
CC antagonist may also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content or other
CC nutritional components. The present sequence represents cDNA encoding a
CC novel human secreted protein. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 97.0%; Score 1305; DB 8; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

```
Qy    1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db   12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy   61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db   72 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 131

Qy  121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db  132 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 191

Qy  181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db  192 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 251

Qy  241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db  252 CAGA-GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 310

Qy  301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db  311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370

Qy  361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db  371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430

Qy  421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db  431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490

Qy  481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db  491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550

Qy  541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db  551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610

Qy  601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
Db  611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670

Qy  660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
Db  671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730

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Qy 1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Qy 1320 TAAAAAAAAAAAAAAAAAAAAAAAA 1345
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RESULT 220
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AC ADD37752;
XX
DT 15-JAN-2004 (first entry)
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DE Human secreted protein encoding sequence #234.
XX
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
XX

OS Homo sapiens.
XX
PN WO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US008279.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-140218/13.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or asthmatic disorders, or related immediate
PT hypersensitivity disorders.
XX
PS Claim 7; SEQ ID NO 234; 1323pp; English.
XX
CC The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or asthmatic disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases , wound healing and disorders of epithelial cell
CC proliferation, immune disorders , cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders , or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein encoding sequence.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 97.0%; Score 1305; DB 9; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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Search completed: June 6, 2004, 10:56:30

Job time : 611.777 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 13:05:30 ; Search time 576.663 Seconds
(without alignments)
10648.235 Million cell updates/sec

Title: US-09-989-724-386
Perfect score: 1346
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 516

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1346	100.0	1346	9	US-09-989-727-386	Sequence 386, App
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512	1324.6	98.4	1447	10	US-09-892-877-22	Sequence 22, Appl
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515	1305	97.0	1356	15	US-10-097-065-122	Sequence 122, App
516	1297	96.4	1312	15	US-10-133-013-205	Sequence 205, App

ALIGNMENTS

RESULT 1
US-09-989-722-386
; Sequence 386, Application US/09989722
; Patent No. US20020072067A1

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-692A-481

Query Match 100.0%; Score 1346; DB 16; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.4e-295;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
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RESULT 508
US-10-140-927-481
; Sequence 481, Application US/10140927
; Publication No. US20040009548A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C180
; CURRENT APPLICATION NUMBER: US/10/140,927
; CURRENT FILING DATE: 2002-05-07
; Prior Apploication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-927-481

Query Match 100.0%; Score 1346; DB 16; Length 1346;

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  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Qy        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900
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Db        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080

Qy       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140

Qy       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 509
US-10-147-536-481
; Sequence 481, Application US/10147536
; Publication No. US20040077064A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C349
; CURRENT APPLICATION NUMBER: US/10/147,536
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-147-536-481

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  Query Match           100.0%;  Score 1346;  DB 17;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-295;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Qy       181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db       181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

Qy       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300

Qy       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy       361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db       361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420

Qy       421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db       421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480

Qy       481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db       481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540

Qy       541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db       541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600

Qy       601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660
Db       601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660

Qy       661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720
Db       661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720

Qy       721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780
Db       721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780

Qy       781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840
Db       781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840

Qy       841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900
Db       841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900

Qy       901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
Db       901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy       961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
Db       961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy      1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
Db      1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080

Qy      1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
Db      1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140

Qy      1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
Db      1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200

Qy      1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
Db      1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260

Qy      1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
Db      1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy      1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
Db      1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 510
US-10-372-876-17
; Sequence 17, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-372-876-17

Query Match 98.5%; Score 1325.4; DB 13; Length 1432;
Best Local Similarity 99.5%; Pred. No. 7e-291;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy         1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db        63 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 122

Qy        61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db       123 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 182

Qy       121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db       183 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 242

Qy       181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db       243 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 302

Qy       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db       303 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 362

Qy       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        363 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 422

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 482

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 542

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 602

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 662

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        663 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 722

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 782

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 842

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 902

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 962

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1022

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1082

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1142

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1202

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1262

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1322

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1382

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |    ||||||||||||||||||||
Db       1383 TGATTGTGAAAAAAAAAAAAAAAAAAAA 1409

RESULT 511
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US-10-097-065-17
; Sequence 17, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
;  APPLICANT: Moore, Paul A. et al.
;  TITLE OF INVENTION: 110 Human Secreted Proteins
;  FILE REFERENCE: PZ021P1
;  CURRENT APPLICATION NUMBER: US/10/097,065
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: PCT/US98/27059
;  PRIOR FILING DATE: 1998-12-17
;  PRIOR APPLICATION NUMBER: 60/070,923
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,007
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,057
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,006
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,369
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,367
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,368
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,169
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,053
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,064
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,054
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,008
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,365
;  PRIOR FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 1432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-097-065-17

  Query Match             98.5%;  Score 1325.4;  DB 15;  Length 1432;
  Best Local Similarity   99.5%;  Pred. No. 7e-291;
  Matches 1340;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 122

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 182

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 242

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 302

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 362

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 422
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Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 482

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 542

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 602

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 662

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        663 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 722

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 782

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 842

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 902

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 962

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1022

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1082

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1142

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1202

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1262

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1322

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1382

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |    ||||||||||||||||||||
Db       1383 TGATTGTGAAAAAAAAAAAAAAAAAA 1409

RESULT 512
US-09-892-877-22
; Sequence 22, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et. al.
;  TITLE OF INVENTION: 97 Human secreted proteins
;  FILE REFERENCE: PZ028P1
;  CURRENT APPLICATION NUMBER: US/09/892,877
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 1447
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-892-877-22

  Query Match            98.4%;  Score 1324.6;  DB 10;  Length 1447;
  Best Local Similarity  99.3%;  Pred. No. 1.1e-290;
  Matches 1338;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899

Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959

Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019

Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079

Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139

Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199

Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259

Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319

Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346

Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAAA 1417


RESULT 513
US-09-948-783-22
; Sequence 22, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et. al.
;  TITLE OF INVENTION: 97 Human secreted proteins
;  FILE REFERENCE: PZ028P2
;  CURRENT APPLICATION NUMBER: US/09/948,783
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,846
;  PRIOR FILING DATE: 2000-09-11
;  PRIOR APPLICATION NUMBER: 09/892,877
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: 09/437,658
;  PRIOR FILING DATE: 1999-11-10
;  PRIOR APPLICATION NUMBER: PCT/US99/09847
;  PRIOR FILING DATE: 1999-05-06
;  PRIOR APPLICATION NUMBER: 60/085,093
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,094
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,105
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,180
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,927
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,906
;  PRIOR FILING DATE: 1998-05-18
;* PRIOR APPLICATION NUMBER: 60/085,924
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,922
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,921
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,923
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,925
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,928
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,920
;  PRIOR FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 465
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 1447
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-948-783-22

  Query Match             98.4%;  Score 1324.6;  DB 10;  Length 1447;
  Best Local Similarity   99.3%;  Pred. No. 1.1e-290;
  Matches 1338;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Db         71 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 130

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180

Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240

Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300

Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420

Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480

Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540

Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600

Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659

Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719

Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |    ||||||||||||||||||||
Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAA 1417


RESULT 514
US-10-372-876-122
; Sequence 122, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
;  APPLICANT: Moore, Paul A. et al.
;  TITLE OF INVENTION: 110 Human Secreted Proteins
;  FILE REFERENCE: PZ021P1
;  CURRENT APPLICATION NUMBER: US/10/372,876
;  CURRENT FILING DATE:  2003-02-26
;  PRIOR APPLICATION NUMBER: 09/334,595
;  PRIOR FILING DATE: 1999-06-17
;  PRIOR APPLICATION NUMBER: PCT/US98/27059
;  PRIOR FILING DATE: 1998-12-17
;  PRIOR APPLICATION NUMBER: 60/070,923
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,007
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,057
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,006
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,369
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,367
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,368
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,169
;  PRIOR FILING DATE: 1997-12-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
;   LENGTH: 1356
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1231)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-372-876-122

  Query Match             97.0%;  Score 1305;  DB 13;  Length 1356;
  Best Local Similarity   99.0%;  Pred. No. 2.9e-286;
  Matches 1333;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    2;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 131

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 191

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 251

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 CAGA-GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 310

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 790

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 850
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Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 910

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 970

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Db        971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Db       1031 AGTGGAGGATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1090

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1150

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              |||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db       1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Db       1271 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCCAAAAA 1330

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAA 1345
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Db       1331 AAAAAAAAAAAAAAAAAAAAAAAAA 1356
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RESULT 515
US-10-097-065-122
; Sequence 122, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1231)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-097-065-122

Query Match 97.0%; Score 1305; DB 15; Length 1356;
Best Local Similarity 99.0%; Pred. No. 2.9e-286;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db         12 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 71

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         72 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 131

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 191

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 251

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 CAGA-GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 310

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        311 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 370

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 430

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        431 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 490

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        491 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 550

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 610

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
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Db        611 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 670

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 730

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 790

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 850
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Qy       840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
Db       851 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 910

Qy       900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
Db       911 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 970

Qy       960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
Db       971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030

Qy      1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
Db      1031 AGTGGAGGATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1090

Qy      1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
Db      1091 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1150

Qy      1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
Db      1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210

Qy      1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
Db      1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270

Qy      1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
Db      1271 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCCAAAAA 1330

Qy      1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1345
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Db      1331 AAAAAAAAAAAAAAAAAAAAAAAAAA 1356
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RESULT 516
US-10-133-013-205
; Sequence 205, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 205
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 2580580cB1
US-10-133-013-205

Query Match 96.4%; Score 1297; DB 15; Length 1312;
Best Local Similarity 99.9%; Pred. No. 1.9e-284;
Matches 1308; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 62

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         63 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 122

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        123 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 182

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        183 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 242

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Db        243 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 302

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 362

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        363 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 422

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        423 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 482

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        483 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 542

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 602

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        603 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 662

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Db        663 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 722

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        723 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 782

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 842

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db        843 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 902

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 962

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1022

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Db       1023 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1082

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Db       1083 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1142

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1143 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1202
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Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1203 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1262

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAA 1308
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Db       1263 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAA 1311
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Search completed: June 6, 2004, 16:41:21
Job time : 772.663 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 07:26:44 ; Search time 258.223 Seconds
(without alignments)
10496.171 Million cell updates/sec

Title: US-09-989-724-386_COPY_7_644
Perfect score: 638
Sequence: 1 atgttgtggctgctcttttt.....atattaatgatgccttcatg 638

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 234

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	100.0	1346	3	AAZ65097	Aaz65097 Membrane-
2	638	100.0	1346	3	AAC58612	Aac58612 Human PRO
3	638	100.0	1346	3	AAA77680	Aaa77680 Human PRO
4	638	100.0	1346	4	AAS21484	Aas21484 Human cDN
5	638	100.0	1346	5	AAF44243	Aaf44243 Human PRO
6	638	100.0	1346	7	ABX77959	Abx77959 Human PRO
7	638	100.0	1346	7	ABX80371	Abx80371 Novel hum
8	638	100.0	1346	7	ACA69277	Aca69277 Human cDN
9	638	100.0	1346	7	ACD24093	Acd24093 Novel hum
10	638	100.0	1346	7	ABX90348	Abx90348 Human sec
11	638	100.0	1346	7	ABX64194	Abx64194 cDNA enco
12	638	100.0	1346	7	ACA67234	Aca67234 cDNA enco
13	638	100.0	1346	7	ACA64416	Aca64416 Novel hum
14	638	100.0	1346	7	ACA03843	Aca03843 cDNA enco
15	638	100.0	1346	7	ABX89381	Abx89381 DNA encod
16	638	100.0	1346	7	ABX80875	Abx80875 Human sec
17	638	100.0	1346	7	ACD44384	Acd44384 cDNA enco
18	638	100.0	1346	7	ACD42035	Acd42035 Human sec
19	638	100.0	1346	7	ABX79555	Abx79555 Human sec
20	638	100.0	1346	7	ACA93576	Aca93576 Novel hum
21	638	100.0	1346	7	ABX81258	Abx81258 Novel hum
22	638	100.0	1346	7	ACA04264	Aca04264 Human cDN
23	638	100.0	1346	7	ACA93074	Aca93074 Novel hum
24	638	100.0	1346	7	ABX17158	Abx17158 Human PRO
25	638	100.0	1346	8	ACA68013	Aca68013 Novel hum
26	638	100.0	1346	8	ACA88462	Aca88462 Human sec
27	638	100.0	1346	8	ACD81969	Acd81969 cDNA enco
28	638	100.0	1346	8	ADA46000	Ada46000 Novel hum
29	638	100.0	1346	8	ADA76431	Ada76431 Human PRO
30	638	100.0	1346	8	ADA19081	Ada19081 Human PRO
31	638	100.0	1346	8	ADA61704	Ada61704 Homo sapi
32	638	100.0	1346	8	ADB19489	Adb19489 Novel hum
33	638	100.0	1346	8	ADB28030	Adb28030 cDNA enco
34	638	100.0	1346	8	ADA86509	Ada86509 Novel hum
35	638	100.0	1346	8	ADB16073	Adb16073 Human PRO
36	638	100.0	1346	8	ADA37897	Ada37897 Human cDN
37	638	100.0	1346	8	ADA47859	Ada47859 Human PRO
38	638	100.0	1346	8	ADA21583	Ada21583 Human cDN
39	638	100.0	1346	8	ADA10370	Ada10370 Human cDN
40	638	100.0	1346	8	ADA67654	Ada67654 Human PRO
41	638	100.0	1346	8	ADB30661	Adb30661 cDNA enco
42	638	100.0	1346	8	ADA85957	Ada85957 Novel hum
43	638	100.0	1346	8	ADA17914	Ada17914 cDNA enco
44	638	100.0	1346	8	ADA97169	Ada97169 Human PRO
45	638	100.0	1346	8	ADA79473	Ada79473 Human PRO
46	638	100.0	1346	8	ADA87612	Ada87612 Novel hum
47	638	100.0	1346	8	ADB16814	Adb16814 Human PRO
48	638	100.0	1346	8	ADA28022	Ada28022 Human cDN
49	638	100.0	1346	8	ADA91906	Ada91906 Novel hum
50	638	100.0	1346	8	ADB14969	Adb14969 Human PRO
51	638	100.0	1346	8	ADB18930	Adb18930 Novel hum
52	638	100.0	1346	8	ADA94145	Ada94145 Human PRO
53	638	100.0	1346	8	ADB20041	Adb20041 Novel hum
54	638	100.0	1346	8	ADB13353	Adb13353 Human PRO
55	638	100.0	1346	8	ACD98664	Acd98664 Novel hum
56	638	100.0	1346	8	ADA94602	Ada94602 Human cDN
57	638	100.0	1346	8	ADA74607	Ada74607 Human PRO
58	638	100.0	1346	8	ADB24840	Adb24840 Human PRO
59	638	100.0	1346	8	ADA82364	Ada82364 Human PRO
60	638	100.0	1346	8	ADA75327	Ada75327 Human PRO
61	638	100.0	1346	8	ADA85405	Ada85405 Novel hum
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63	638	100.0	1346	8	ADB30109	Adb30109 cDNA enco
64	638	100.0	1346	8	ADA80637	Ada80637 Human PRO
65	638	100.0	1346	8	ADA75879	Ada75879 Human PRO
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67	638	100.0	1346	8	ADA47104	Ada47104 Human PRO
68	638	100.0	1346	8	ADB25400	Adb25400 Human PRO
69	638	100.0	1346	8	ADA93576	Ada93576 Human PRO
70	638	100.0	1346	8	ADB26926	Adb26926 cDNA enco
71	638	100.0	1346	8	ADB31213	Adb31213 cDNA enco
72	638	100.0	1346	8	ADA92948	Ada92948 Human cDN
73	638	100.0	1346	8	ADA61141	Ada61141 Homo sapi
74	638	100.0	1346	8	ADB24288	Adb24288 Human PRO
75	638	100.0	1346	8	ADA96617	Ada96617 Human PRO
76	638	100.0	1346	8	ADA81189	Ada81189 Human PRO
77	638	100.0	1346	8	ADA96065	Ada96065 Human PRO
78	638	100.0	1346	8	ADB26374	Adb26374 cDNA enco
79	638	100.0	1346	8	ADB21859	Adb21859 Novel hum
80	638	100.0	1346	8	ADA77638	Ada77638 Human PRO
81	638	100.0	1346	8	ADB18378	Adb18378 cDNA enco
82	638	100.0	1346	8	ADA87061	Ada87061 Novel hum
83	638	100.0	1346	8	ADA88164	Ada88164 Novel hum
84	638	100.0	1346	8	ADA46552	Ada46552 Novel hum
85	638	100.0	1346	8	ADB28582	Adb28582 cDNA enco
86	638	100.0	1346	8	ADB29134	Adb29134 cDNA enco
87	638	100.0	1346	8	ACH65530	Ach65530 Human cDN
88	638	100.0	1346	8	ADA77086	Ada77086 Human PRO
89	638	100.0	1346	8	ADA22509	Ada22509 Human cDN
90	638	100.0	1346	8	ADA88716	Ada88716 Novel hum
91	638	100.0	1346	8	ADA97721	Ada97721 Human PRO
92	638	100.0	1346	8	ADB27478	Adb27478 cDNA enco
93	638	100.0	1346	8	ADB22411	Adb22411 Novel hum
94	638	100.0	1346	8	ACD39520	Acd39520 Human cDN
95	638	100.0	1346	8	ADA06675	Ada06675 Human sec
96	638	100.0	1346	8	ADA39368	Ada39368 Human cDN

97	638	100.0	1346	8	ADA67102	Ada67102	Human PRO
98	638	100.0	1346	8	ADB22963	Adb22963	Human PRO
99	638	100.0	1346	8	ADB23736	Adb23736	Human PRO
100	638	100.0	1346	8	ADA92458	Ada92458	Novel hum
101	638	100.0	1346	8	ADB15521	Adb15521	Human PRO
102	638	100.0	1346	8	ADB38773	Adb38773	Novel hum
103	638	100.0	1346	8	ADB96394	Adb96394	Human PRO
104	638	100.0	1346	8	ADB38221	Adb38221	Novel hum
105	638	100.0	1346	9	ADB66693	Adb66693	Novel hum
106	638	100.0	1346	9	ADB89773	Adb89773	Human PRO
107	638	100.0	1346	9	ADB90505	Adb90505	Human PRO
108	638	100.0	1346	9	ADB39606	Adb39606	Novel hum
109	638	100.0	1346	9	ADB47229	Adb47229	Novel hum
110	638	100.0	1346	9	ADB86836	Adb86836	Human PRO
111	638	100.0	1346	9	ADB77441	Adb77441	Novel hum
112	638	100.0	1346	9	ADB34598	Adb34598	Human PRO
113	638	100.0	1346	9	ADB35702	Adb35702	Human PRO
114	638	100.0	1346	9	ADB34046	Adb34046	Human PRO
115	638	100.0	1346	9	ADB35150	Adb35150	Human PRO
116	638	100.0	1346	9	ADB36254	Adb36254	Human PRO
117	638	100.0	1346	9	ADB46649	Adb46649	Novel hum
118	638	100.0	1346	9	ADC57866	Adc57866	Human PRO
119	638	100.0	1346	9	ADC55230	Adc55230	Human PRO
120	638	100.0	1346	9	ADC12097	Adc12097	Human cDN
121	638	100.0	1346	9	ADC56519	Adc56519	Human PRO
122	638	100.0	1346	9	ADC07574	Adc07574	Human cDN
123	638	100.0	1346	9	ADC11564	Adc11564	Human cDN
124	638	100.0	1346	9	ADC50522	Adc50522	Novel hum
125	638	100.0	1346	9	ADC72069	Adc72069	Novel hum
126	638	100.0	1346	9	ADC60048	Adc60048	Novel hum
127	638	100.0	1346	9	ADC53055	Adc53055	Novel hum
128	638	100.0	1346	9	ADC57409	Adc57409	Novel hum
129	638	100.0	1346	9	ADC60600	Adc60600	Novel hum
130	638	100.0	1346	9	ADC51075	Adc51075	Novel hum
131	638	100.0	1346	9	ADC65602	Adc65602	Human PRO
132	638	100.0	1346	9	ADC54700	Adc54700	Novel hum
133	638	100.0	1346	9	ADC53661	Adc53661	Novel hum
134	638	100.0	1346	9	ADC59184	Adc59184	Novel hum
135	638	100.0	1346	9	ADC56062	Adc56062	Novel hum
136	638	100.0	1346	9	ADC58632	Adc58632	Novel hum
137	638	100.0	1346	9	ADC14686	Adc14686	Novel hum
138	638	100.0	1346	9	ADD08218	Add08218	Novel hum
139	638	100.0	1346	9	ADD03306	Add03306	Novel hum
140	638	100.0	1346	9	ADC90298	Adc90298	Novel hum
141	638	100.0	1346	9	ADC82043	Adc82043	Human PRO
142	638	100.0	1346	9	ADC69717	Adc69717	cDNA enco
143	638	100.0	1346	9	ADC48606	Adc48606	Human PRO
144	638	100.0	1346	9	ADD10135	Add10135	Human PRO
145	638	100.0	1346	9	ADD07685	Add07685	Novel hum
146	638	100.0	1346	9	ADD04710	Add04710	Novel hum
147	638	100.0	1346	9	ADC82576	Adc82576	Human PRO
148	638	100.0	1346	9	ADC80666	Adc80666	Novel hum
149	638	100.0	1346	9	ADD11173	Add11173	Human PRO
150	638	100.0	1346	9	ADC48054	Adc48054	Human PRO
151	638	100.0	1346	9	ADD08756	Add08756	Novel hum
152	638	100.0	1346	9	ADC80114	Adc80114	Novel hum
153	638	100.0	1346	9	ADD07005	Add07005	Novel hum
154	638	100.0	1346	9	ADD09583	Add09583	Human PRO
155	638	100.0	1346	9	ADC83252	Adc83252	Human PRO
156	638	100.0	1346	9	ADD41296	Add41296	Novel hum
157	638	100.0	1346	9	ADD52435	Add52435	cDNA enco
158	638	100.0	1346	9	ADD53175	Add53175	cDNA enco
159	638	100.0	1346	9	ADD53727	Add53727	Novel hum
160	638	100.0	1346	9	ADD55359	Add55359	Human PRO
161	638	100.0	1346	9	ADD56317	Add56317	Human PRO
162	638	100.0	1346	9	ADD51883	Add51883	cDNA enco
163	638	100.0	1346	9	ADD02682	Add02682	Human PRO
164	638	100.0	1346	9	ADD02116	Add02116	Human PRO
165	638	100.0	1346	9	ADD54298	Add54298	Novel hum
166	638	100.0	1346	9	ADD54755	Add54755	Human PRO
167	638	100.0	1346	9	ADD92615	Add92615	Human PRO
168	638	100.0	1346	9	ADD91511	Add91511	Human PRO
169	638	100.0	1346	9	ADE04125	Ade04125	Human PRO
170	638	100.0	1346	9	ADE26909	Ade26909	Novel hum
171	638	100.0	1346	9	ADE32422	Ade32422	Novel hum
172	638	100.0	1346	9	ADE22354	Ade22354	cDNA enco
173	638	100.0	1346	9	ADD79578	Add79578	cDNA enco
174	638	100.0	1346	9	ADE42114	Ade42114	Human PRO
175	638	100.0	1346	9	ADE17931	Ade17931	Human PRO
176	638	100.0	1346	9	ADD92063	Add92063	Human PRO
177	638	100.0	1346	9	ADE33526	Ade33526	Novel hum
178	638	100.0	1346	9	ADE34078	Ade34078	Novel hum
179	638	100.0	1346	9	ADD80130	Add80130	cDNA enco
180	638	100.0	1346	9	ADD93167	Add93167	Human PRO
181	638	100.0	1346	9	ADE19587	Ade19587	Human PRO
182	638	100.0	1346	9	ADE19035	Ade19035	Human PRO
183	638	100.0	1346	9	ADE43231	Ade43231	Human PRO
184	638	100.0	1346	9	ADD96020	Add96020	Human PRO
185	638	100.0	1346	9	ADE22906	Ade22906	cDNA enco
186	638	100.0	1346	9	ADD79024	Add79024	cDNA enco
187	638	100.0	1346	9	ADE26376	Ade26376	Novel hum
188	638	100.0	1346	9	ADE32974	Ade32974	Novel hum
189	638	100.0	1346	9	ADE42666	Ade42666	Human PRO
190	638	100.0	1346	9	ADD80682	Add80682	cDNA enco
191	638	100.0	1346	9	ADD89710	Add89710	Human PRO
192	638	100.0	1346	9	ADE40994	Ade40994	Human PRO
193	638	100.0	1346	9	ADE04793	Ade04793	Human PRO
194	638	100.0	1346	10	ADC81218	Adc81218	Novel hum
195	638	100.0	1346	10	ADD76666	Add76666	Human PRO
196	638	100.0	1346	10	ADD88030	Add88030	Human PRO
197	638	100.0	1346	10	ADD86434	Add86434	Human PRO
198	638	100.0	1346	10	ADE75882	Ade75882	Human PRO
199	638	100.0	1346	10	ADE23458	Ade23458	cDNA enco
200	638	100.0	1346	10	ADE24010	Ade24010	cDNA enco
201	638	100.0	1346	10	ADE24653	Ade24653	cDNA enco
202	638	100.0	1346	10	ADD87478	Add87478	Human PRO
203	638	100.0	1346	10	ADE89344	Ade89344	Human PRO
204	638	100.0	1346	10	ADE18483	Ade18483	Human PRO
205	638	100.0	1346	10	ADE88792	Ade88792	Human PRO
206	627	98.3	666	4	AAF94460	Aaf94460	Human hyd
207	627	98.3	1347	4	AAF94470	Aaf94470	Human hyd
208	627	98.3	1432	7	ADA56090	Ada56090	Gene enco
209	627	98.3	1432	7	ADA39900	Ada39900	Human sec
210	627	98.3	1432	8	ADA11489	Ada11489	Human cDN
211	627	98.3	1432	9	ADD37613	Add37613	Human sec
212	626.6	98.2	1447	3	AAZ65261	Aaz65261	Human sec
213	626.6	98.2	1447	9	ADE11650	Ade11650	Human sec
214	625.4	98.0	1345	7	ABZ78127	Abz78127	Human can
215	625.4	98.0	1401	2	AAV40540	Aav40540	Homo sapi
216	625	98.0	848	2	AAX19983	Aax19983	Human sec
217	625	98.0	848	2	AAX39430	Aax39430	Human sec
218	625	98.0	848	2	AAX41369	Aax41369	Extended
219	625	98.0	848	2	AAX97564	Aax97564	Extended
220	625	98.0	848	2	AAZ40770	Aaz40770	Secreted
221	625	98.0	848	2	AAX26672	Aax26672	Extended
222	625	98.0	848	2	AAX51777	Aax51777	Human sec
223	625	98.0	848	2	AAX51449	Aax51449	Human sec
224	625	98.0	848	2	AAX40428	Aax40428	Extended
225	625	98.0	848	3	AAZ42251	Aaz42251	Human ful
226	625	98.0	848	3	AAC00012	Aac00012	Human sec
227	624.4	97.9	848	2	AAX88191	Aax88191	Human sec
228	623.4	97.7	847	2	AAX30083	Aax30083	Human sec
C 229	616	96.6	1365	4	AAH98224	Aah98224	Human EST
230	615	96.4	1356	2	AAX97957	Aax97957	Human sec
231	615	96.4	1356	7	ADA56545	Ada56545	Gene enco
232	615	96.4	1356	7	ADA40381	Ada40381	Human sec
233	615	96.4	1356	8	ADA11594	Ada11594	Human cDN
234	615	96.4	1356	9	ADD37752	Add37752	Human sec

ALIGNMENTS

RESULT 1
AAZ65097
ID AAZ65097 standard; cDNA; 1346 BP.

PT stimulating release of TNF-alpha from human blood.
XX
PS Claim 2; SEQ ID NO 481; 638pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 638; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.1e-184;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638
              |||||||||||||||||||||||||||||||||||||
Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644
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RESULT 206
AAF94460
ID AAF94460 standard; cDNA; 666 BP.
XX
AC AAF94460;
XX
DT 04-JUN-2001 (first entry)
XX
DE Human hydrophobic domain containing protein clone HP10720 cDNA #74.
XX
KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW behavioural characteristic; immune response; ss.
XX
OS Homo sapiens.
XX
PN WO200112660-A2.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000WO-JP005356.
XX
PR 17-AUG-1999; 99JP-00230344.
PR 07-SEP-1999; 99JP-00252551.
PR 01-OCT-1999; 99JP-00281132.
PR 22-OCT-1999; 99JP-00301624.
PR 04-NOV-1999; 99JP-00313877.
XX
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-160059/16.
DR P-PSDB; AAB88580.
XX
PT Human proteins with hydrophobic domains and the DNAs which encode them
PT are useful for treating autoimmune disorders, burns and tumors and for
PT screening novel pharmaceuticals.
XX
PS Claim 3; Page 368; 518pp; English.
XX
CC AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC for genetic diagnosis and gene sources for gene therapy or for producing
CC (I) in large quantities. Cells containing (II) are used for the detection
CC of ligands or receptors corresponding to membrane or secretory proteins
CC and to screen small molecule novel pharmaceuticals. Antibodies directed
CC to (I) can be used for the detection, quantification and purification of
CC (I). Activities of (I) may include cytokine and cell

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CC   proliferation/differentiation function, immune stimulating or suppressing
CC   activity, haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC   activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC   multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC   inflammatory bowel disease and tumours. (I) and (II) can also be used for
CC   wound healing, as nutritional sources or supplements e.g. as amino acid,
CC   carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC   processing and utilisation of dietary fat, protein, carbohydrate,
CC   vitamins and minerals, to effect behavioural characteristics, to affect
CC   appetite, and can act as antigens in vaccines to raise an immune response
CC   to the protein or another material cross-reactive with the protein
XX
SQ   Sequence 666 BP; 203 A; 148 C; 136 G; 179 T; 0 U; 0 Other;

  Query Match             98.3%;  Score 627;  DB 4;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-181;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        601 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 639


RESULT 207
AAF94470
ID   AAF94470 standard; cDNA; 1347 BP.
XX
AC   AAF94470;
XX
DT   04-JUN-2001  (first entry)
XX
DE   Human hydrophobic domain containing protein clone HP10720 cDNA #84.
XX
KW   Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW   antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW   cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW   HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW   inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW   behavioural characteristic; immune response; ss.
XX
OS   Homo sapiens.
XX
PN   WO200112660-A2.
XX
PD   22-FEB-2001.
XX
PF   10-AUG-2000; 2000WO-JP005356.
XX
PR   17-AUG-1999;   99JP-00230344.
PR   07-SEP-1999;   99JP-00252551.
PR   01-OCT-1999;   99JP-00281132.
PR   22-OCT-1999;   99JP-00301624.
PR   04-NOV-1999;   99JP-00313877.
XX
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2001-160059/16.
DR   P-PSDB; AAB88580.
XX
PT   Human proteins with hydrophobic domains and the DNAs which encode them
PT   are useful for treating autoimmune disorders, burns and tumors and for
PT   screening novel pharmaceuticals.
XX
PS   Claim 4; Page 384-386; 518pp; English.
XX
CC   AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC   AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC   anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC   osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC   in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC   prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC   for genetic diagnosis and gene sources for gene therapy or for producing
CC   (I) in large quantities. Cells containing (II) are used for the detection
CC   of ligands or receptors corresponding to membrane or secretory proteins
CC   and to screen small molecule novel pharmaceuticals. Antibodies directed
CC   to (I) can be used for the detection, quantification and purification of
CC   (I). Activities of (I) may include cytokine and cell
CC   proliferation/differentiation function, immune stimulating or suppressing
CC   activity, haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC   activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC   multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC   inflammatory bowel disease and tumours. (I) and (II) can also be used for
CC   wound healing, as nutritional sources or supplements e.g. as amino acid,
CC   carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC   processing and utilisation of dietary fat, protein, carbohydrate,
CC   vitamins and minerals, to effect behavioural characteristics, to affect
CC   appetite, and can act as antigens in vaccines to raise an immune response
CC   to the protein or another material cross-reactive with the protein
XX
SQ   Sequence 1347 BP; 434 A; 252 C; 243 G; 418 T; 0 U; 0 Other;

  Query Match             98.3%;  Score 627;  DB 4;  Length 1347;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-181;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 85
```

```
Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        86 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 145

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       146 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 205

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       206 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 265

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       266 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 325

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       326 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 385

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       386 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 445

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       446 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 505

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       506 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 565

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       566 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 625

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
             ||||||||||||||| ||||||||||||||||||||||||
Db       626 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 664
```

RESULT 208
ADA56090
ID ADA56090 standard; DNA; 1432 BP.
XX
AC ADA56090;
XX
DT 20-NOV-2003 (first entry)
XX
DE Gene encoding human secreted protein #269.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR P-PSDB; ADA56986.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 21; SEQ ID NO 279; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.3%; Score 627; DB 7; Length 1432;
Best Local Similarity 99.8%; Pred. No. 2.7e-181;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy         1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        69 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 128

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       129 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 188

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       189 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 248

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       249 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 308

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       309 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 368

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        369 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 428

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 488

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 548

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 608

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 668

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        669 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 707
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RESULT 209
ADA39900
ID   ADA39900 standard; cDNA; 1432 BP.
XX
AC   ADA39900;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human secreted protein encoding cDNA.
XX
KW   Human; secreted protein; cancer; hyperproliferative disorder;
KW   rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW   anaemia; allergic reaction; asthma; cardiovascular disorder;
KW   wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW   antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW   vulnerary; cardiant; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO2002102993-A2.
XX
PD   27-DEC-2002.
XX
PF   19-MAR-2002; 2002WO-US008123.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-175238/17.
XX
PT   New human secreted proteins and nucleic acid molecules, useful for
PT   preparing a diagnostic or pharmaceutical composition for diagnosing,
PT   preventing or treating cancer or other hyperproliferative disorder,
PT   asthma, allergies or AIDS.
XX
PS   Claim 9; SEQ ID NO 282; 3205pp; English.
XX
CC   The invention relates to novel genes ADA39629-ADA40565 and proteins
CC   ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC   treating or ameliorating medical conditions e.g. by protein or gene
CC   therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC   fragments, and agonists or antagonists that bind to the polypeptide are
CC   useful for preparing a diagnostic or pharmaceutical composition for
CC   diagnosing or treating cancer or other hyperproliferative disorder. The
CC   polypeptides and nucleic acid molecules are also useful for detecting,
CC   preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC   or other hyperproliferative disorders including neoplasms, autoimmune
CC   disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC   erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC   anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC   thrombocytopenia), allergic reactions including asthma or eczema,
CC   inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC   bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC   Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC   (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC   fungal or viral infections including HIV/AIDS), or wound healing and
CC   disorders of epithelial cell proliferation. The nucleic acids are also
CC   useful for chromosome identification, radiation hybrid mapping or long-
CC   range restriction mapping, as molecular weight markers, or as
CC   hybridization or diagnostic probes. The polypeptides and antibodies are
CC   useful for providing immunological probes for differential identification
CC   of the tissues immunohistochemistry assays. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

  Query Match             98.3%;  Score 627;  DB 7;  Length 1432;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-181;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 128

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 188

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 248

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 308

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 368

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 428

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 488

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 548

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 608

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 668

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        669 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 707
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RESULT 210

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ADA11489
ID   ADA11489 standard; DNA; 1432 BP.
XX
AC   ADA11489;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
XX
KW   cancer; inflammation; immune disorder; neurological disorder;
KW   blood clotting disorder; food additive; food preservative;
KW   storage capability; fat content; nutritional component; ds; gene; human.
XX
OS   Homo sapiens.
XX
PN   US2003055236-A1.
XX
PD   20-MAR-2003.
XX
PF   14-MAR-2002; 2002US-00097065.
XX
PR   18-DEC-1997;   97US-0068006P.
PR   18-DEC-1997;   97US-0068007P.
PR   18-DEC-1997;   97US-0068008P.
PR   18-DEC-1997;   97US-0068053P.
PR   18-DEC-1997;   97US-0068054P.
PR   18-DEC-1997;   97US-0068057P.
PR   18-DEC-1997;   97US-0068064P.
PR   18-DEC-1997;   97US-0070923P.
PR   19-DEC-1997;   97US-0068169P.
PR   19-DEC-1997;   97US-0068365P.
PR   19-DEC-1997;   97US-0068367P.
PR   19-DEC-1997;   97US-0068368P.
PR   19-DEC-1997;   97US-0068369P.
PR   17-DEC-1998;   98WO-US027059.
PR   17-JUN-1999;   99US-00334595.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA,  Ruben SM,  Carter KC,  Shi Y,  Rosen CA,  Soppet DR;
PI   Kyaw H,  Wei Y,  Florence KA,  Duan DR,  Florence C,  Greene JM,  Feng P;
PI   Ferrie AM,  Yu G,  Janat P,  Ni J;
XX
DR   WPI; 2003-567105/53.
DR   P-PSDB; ADA11613.
XX
PT   New secreted HKABT24 nucleic acid molecules and polypeptides, useful for
PT   preventing, treating, or ameliorating a medical condition, such as
PT   cancer, inflammation, immune disorders, neurological and blood clotting
PT   disorders.
XX
PS   Claim 1; SEQ ID NO 17; 118pp; English.
XX
CC   The invention relates to an isolated HKABT24 nucleic acid molecule. The
CC   polypeptides, nucleic acids and antibodies are useful for diagnosing a
CC   pathological condition or a susceptibility to a pathological condition,
CC   for preventing, treating, or ameliorating a medical condition, such as
CC   cancer, inflammation and other immune disorders, neurological and blood
CC   clotting disorders. The nucleic acids are also useful for chromosome
CC   identification, radiation hybrid mapping or long-range restriction
CC   mapping. The polypeptides and antibodies are useful for providing
CC   immunological probes for differential identification of the tissues
CC   immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
CC   antagonist may also be used as a food additive or preservative to
CC   increase or decrease storage capabilities, fat content or other
CC   nutritional components. The present sequence represents cDNA encoding a
CC   novel human secreted protein. Note: The sequence data for this patent did
CC   not form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
CC   seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
XX
SQ   Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;
```

```
  Query Match             98.3%;  Score 627;  DB 8;  Length 1432;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-181;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 128

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 188

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 248

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 308

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 368

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 428

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 488

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 548

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 608

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 668

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        669 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 707
```

```
RESULT 211
ADD37613
ID   ADD37613 standard; cDNA; 1432 BP.
XX
AC   ADD37613;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human secreted protein encoding sequence #95.
XX
KW   human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
KW   Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200290526-A2.
XX
PD   14-NOV-2002.
XX
PF   19-MAR-2002; 2002WO-US008279.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
```

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-140218/13.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or asthmatic disorders, or related immediate
PT hypersensitivity disorders.
XX
PS Claim 7; SEQ ID NO 95; 1323pp; English.
XX
CC The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or asthmatic disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases , wound healing and disorders of epithelial cell
CC proliferation, immune disorders , cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders , or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein encoding sequence.
XX
SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.3%; Score 627; DB 9; Length 1432;
Best Local Similarity 99.8%; Pred. No. 2.7e-181;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 128

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 188

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 248

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 308

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 368

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 428

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 488

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 548

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 608

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 668

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        669 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 707
```

RESULT 212
AAZ65261
ID AAZ65261 standard; DNA; 1447 BP.
XX
AC AAZ65261;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human secreted protein gene 12.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9958660-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009847.
XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R;
XX
DR WPI; 2000-062296/05.
DR P-PSDB; AAY76135.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 303; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed

CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 97 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.2%; Score 626.6; DB 3; Length 1447;
Best Local Similarity 99.7%; Pred. No. 3.6e-181;
Matches 637; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 136

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 556

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 715
```

RESULT 213
ADE11650
ID ADE11650 standard; cDNA; 1447 BP.
XX
AC ADE11650;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted polypeptide cDNA #12.
XX
KW Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
KW Alzheimer's disease; human; ss; gene.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003100051-A1.
XX
PD 29-MAY-2003.
XX
PF 10-SEP-2001; 2001US-00948783.
XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 18-MAY-1998; 98US-0085928P.
PR 06-MAY-1999; 99WO-US009847.
PR 10-NOV-1999; 99US-00437658.
PR 11-SEP-2000; 2000US-0231846P.
PR 28-JUN-2001; 2001US-00892877.
XX
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
XX
PI Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R, Birse CE;
XX
DR WPI; 2003-801210/75.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX
PS Claim 1; SEQ ID NO 22; 453pp; English.
XX
CC The invention relates to human secreted polypeptides and the
CC polynucleotides encoding them. The sequences are useful for preparing
CC medicaments for preventing, treating or ameliorating medical conditions
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC as Alzheimer's disease. This sequence represents cDNA encoding a human
CC secreted polypeptide of the invention.
XX
SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.2%; Score 626.6; DB 9; Length 1447;
Best Local Similarity 99.7%; Pred. No. 3.6e-181;
Matches 637; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```
Qy        1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       77 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 136

Qy       61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy      121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy      181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy      241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy      301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db      377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy      361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy      421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      497 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 556

Qy      481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy      541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy      601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
            |||||||||||||| ||||||||||||||||||||||||
Db      677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 715
```

RESULT 214
ABZ78127
ID ABZ78127 standard; cDNA; 1345 BP.
XX
AC ABZ78127;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related coding sequence, 156P1D4.
XX
KW Human; cytostatic; vaccine; cancer; immune response; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
DR P-PSDB; ABR01796.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 26; Fig 2G; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. 74P3B3 maps
CC to chromosome 8p21.3-p22, 83P4B8 maps to chromosome 15q25.1, 109P1D4 maps
CC to chromosome Xq21.3, 151P1C7A maps to chromosome 10q11.2, 151P4E11 maps
CC to chromosome 11q13.3-q13.5, 154P2A8 maps to chromosome 3q24, 156P1D4
CC maps to chromosome Xp22.3, 156P5C12 maps to chromosome 2p13.1-p12,
CC 159P2B5 maps to chromosome 7p15.1, 161P2B7A maps to chromosome 3q25-q26,
CC 179P3G7 maps to chromosome 12q12-q13, 184P3C10B maps to chromosome
CC 19p13.1, 184P3G10 maps to chromosome 2p12, 185P2C9 maps to chromosome
CC 18p11.22, 185P3C2 maps to chromosome 17q21, 186P1H9 maps to chromosome
CC 7q21.3-q22.1, 187P3F2 maps to chromosome 3p14.2 and 192P2G7 maps to
CC chromosome 22q13.2-q13.31
XX
SQ Sequence 1345 BP; 435 A; 251 C; 241 G; 418 T; 0 U; 0 Other;

Query Match 98.0%; Score 625.4; DB 7; Length 1345;
Best Local Similarity 99.7%; Pred. No. 8.2e-181;
Matches 637; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy        1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       24 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 83

Qy       61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       84 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 143

Qy      121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      144 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 203

Qy      181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      204 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 263

Qy      241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      264 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAA 323

Qy      301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      324 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 383

Qy      361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      384 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 443

Qy      421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      444 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 503

Qy      481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      504 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 563
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 623

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| |||||||||||||||||||||||||
Db        624 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 662
```

RESULT 215
AAV40540
ID AAV40540 standard; cDNA; 1401 BP.
XX
AC AAV40540;
XX
DT 09-NOV-1998 (first entry)
XX
DE Homo sapiens secreted protein clone AM42_3.
XX
KW Clone; secreted protein; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 71. .739
FT /*tag= a
FT /note= "secreted protein"
XX
PN WO9832853-A2.
XX
PD 30-JUL-1998.
XX
PF 23-JAN-1998; 98WO-US001396.
XX
PR 24-JAN-1997; 97US-00788789.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-427949/36.
DR P-PSDB; AAW29670.
XX
PT New isolated polynucleotide(s) and secreted proteins - isolated from
PT human foetal kidney, adult brain, adult salivary gland, foetal brain and
PT adult testes cDNA libraries.
XX
PS Claim 16; Page 64-65; 109pp; English.
XX
CC The sequence is that of encoding a secreted protein. Such a protein can
CC have biological activities, e.g. nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity, and other activities
XX
SQ Sequence 1401 BP; 458 A; 258 C; 251 G; 434 T; 0 U; 0 Other;

Query Match 98.0%; Score 625.4; DB 2; Length 1401;
Best Local Similarity 99.7%; Pred. No. 8.3e-181;
Matches 637; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 130

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 190

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 250

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 310

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 370

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        371 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTAAATGAC 430

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 490

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 550

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 610

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 670

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| |||||||||||||||||||||||||
Db        671 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 709
```

RESULT 216
AAX19983
ID AAX19983 standard; cDNA; 848 BP.
XX
AC AAX19983;
XX
DT 16-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO:27.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906439-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001233.
XX
PR 01-AUG-1997; 97US-00904468.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153700/13.
DR P-PSDB; AAY04156.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA

PT libraries derived from liver, lung, large intestine, colon, thyroid and
PT pancreas tissue.
XX
PS Example 28; Page 157-158; 398pp; English.
XX
CC AAX40251 to AAX40397 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY11533 to
CC AAY11679, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC present sequence represents a 5' EST from an example of the present
CC invention
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |||||||||||||||||||||||||||:|||:||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
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Db 632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670

RESULT 217
AAX39430
ID AAX39430 standard; DNA; 848 BP.
XX
AC AAX39430;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO: 27.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906551-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001235.
XX
PR 01-AUG-1997; 97US-00905133.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153781/13.
DR P-PSDB; AAW93620, AAY11373.
XX
PT New nucleic acids encoding human secreted - proteins obtained from cDNA
PT libraries prepared from substantia nigra, cerebellum, surrenals and fetal
PT brain tissue.
XX
PS Example 28; Page 157-158; 434pp; English.
XX
CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY11374 to
CC AAY11531, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. This
CC sequence encodes the human 5' EST secreted proteins represented in
CC AAW93620 and AAY11373
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91
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Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 218
AAX41369
ID AAX41369 standard; cDNA; 848 BP.
XX
AC AAX41369;
XX
DT 22-JUN-1999 (first entry)
XX
DE Extended cDNA obtained from 5' EST, SEQ ID NO: 27 from WO 9906553.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; antiinflammatory; tumour inhibition; antitumour; ds.
XX
OS Homo sapiens.
XX
PN WO9906553-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001237.
XX
PR 01-AUG-1997; 97US-00905051.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153783/13.
DR P-PSDB; AAY12520.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries derived from umbilical cord, lymph ganglia, lymphocytes and
PT placental tissue.
XX
PS Example 28; Page 156-157; 411pp; English.
XX
CC The patent relates to sequences of 5' ESTs derived from mRNAs encoding
CC secreted proteins. The nucleic acid sequences can be used for producing
CC secreted human gene products. They can also be used to develop products
CC for diagnosis and therapy. The proteins obtained may have cytokine
CC activity, cell proliferation/differentiation activity, haematopoiesis
CC regulating activity, tissue growth regulating activity, reproductive
CC hormone regulating activity, chemotactic/ chemokinetic activity,
CC haemostatic and thrombolytic activity, receptor/ ligand activity,
CC antiinflammatory activity, tumour inhibition activity or other
CC activities. The products can be used in forensic, gene therapy and
CC chromosome mapping procedures. The sequences can also be used for
CC obtaining corresponding promoter sequences. The nucleic acids encoding
CC the signal peptide can be used for directing extracellular secretion of a
CC polypeptide or the insertion of a polypeptide into a membrane, or
CC importing a polypeptide into a cell
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy         1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
Db        32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

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RESULT 219
AAX97564
ID   AAX97564 standard; DNA; 848 BP.
XX
AC   AAX97564;
XX
DT   13-SEP-1999  (first entry)
XX
DE   Extended human secreted protein coding sequence, SEQ ID NO. 27.
XX
KW   Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW   cellular differentiation; immune system regulator; anti-inflammatory;
KW   haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW   reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW   genetic disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9931236-A2.
XX
PD   24-JUN-1999.
XX
PF   17-DEC-1998;   98WO-IB002122.
XX
PR   17-DEC-1997;   97US-0069957P.
PR   09-FEB-1998;   98US-0074121P.
PR   13-APR-1998;   98US-0081563P.
PR   10-AUG-1998;   98US-0096116P.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L,  Duclert A,  Dumas Milne Edwards J;
XX
DR   WPI; 1999-385906/32.
DR   P-PSDB; AAY35890, AAY35891.
XX
PT   New isolated human secreted proteins.
XX
PS   Example 28; Page 165-166; 516pp; English.
XX
CC   This sequence represents an extended human secreted protein coding
CC   sequence of the invention. The secreted proteins can be used in treating
CC   or controlling a variety of human conditions. The secreted proteins may
CC   act as cytokines or may affect cellular proliferation or differentiation
CC   or may act as immune system regulators, haematopoiesis regulators, tissue
CC   growth regulators, regulators of reproductive hormones or cell movement
CC   or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC   tumour inhibition activity. The DNAs can be used in forensic procedures
CC   to identify individuals or in diagnostic procedures to identify
CC   individuals having genetic diseases resulting from abnormal expression of
CC   the genes corresponding to the extended cDNAs. They are also useful for
CC   constructing a high resolution map of the human chromosomes. They can
CC   also be used for gene therapy to control or treat genetic diseases
XX
SQ   Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

  Query Match             98.0%;  Score 625;  DB 2;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 8.7e-181;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 220
AAZ40770
ID   AAZ40770 standard; DNA; 848 BP.
XX
AC   AAZ40770;
XX
DT   18-JAN-2000  (first entry)
XX
DE   Secreted protein extended EST coding sequence #6.
XX
KW   Secreted protein; fingerprint identification technique;
KW   chromosome mapping; human; hereditary disease; diagnosis; cancer;
KW   hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy;
KW   autoimmune disease; rheumatic disease; embryogenic disorder; myopathy;
KW   renal injury; amino aciduria; hypoglycaemia; male rat infertility;
KW   hypertension; ss.
XX
OS   Homo sapiens.
XX
PN   WO9940189-A2.
XX
PD   12-AUG-1999.
XX
PF   09-FEB-1999;   99WO-IB000282.
XX
PR   09-FEB-1998;   98US-0074121P.
PR   13-APR-1998;   98US-0081563P.
PR   10-AUG-1998;   98US-0096116P.
PR   04-SEP-1998;   98US-0099273P.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L,  Duclert A,  Dumas Milne Edwards J;
XX
DR   WPI; 1999-600966/51.
DR   P-PSDB; AAY59652, AAY59653.
XX
PT   Extended cDNAs useful for expressing secreted proteins and to obtain
PT   specific antibodies.
```

XX
PS Example 28; Page 141-142; 244pp; English.
XX
CC This sequence represents a portion of a nucleic acid sequence of the
CC invention. The invention relates to 70 nucleic acids encoding human
CC secreted proteins. The extended cDNAs (or genomic DNAs obtainable from
CC them) may be used to prepare PCR primers and probes. These are useful for
CC forensic matching or positive identification by DNA sequencing. They may
CC also be used in alternative fingerprint identification techniques.
CC Antibodies against the proteins encoded by the extended cDNAs are useful
CC in identification of tissue types or cell species, as well as identifying
CC tissue specific soluble proteins. The sequences can be used for
CC chromosome mapping and identification of genes associated with hereditary
CC diseases or drug response. signal sequences from the cDNAs can be used in
CC construction of secretion vectors. Other sequences derived from the
CC extended cDNAs can be used to clone upstream genomic DNA sequences
CC including promoters. This is in turn useful for identifying proteins that
CC interact with promoter sequences. Some of the proteins may be useful in
CC diagnosing and treating several disorders including, but not limited to:
CC cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders,
CC autoimmune diseases, and rheumatic diseases, embryogenic disorders,
CC hypertension, renal injury, amino acidurias, hypoglycaemia, male rat
CC infertility and myopathies
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 221
AAX26672
ID AAX26672 standard; RNA; 848 BP.
XX
AC AAX26672;
XX
DT 18-JUN-1999 (first entry)
XX
DE Extended cDNA derived from a 5' EST encoding a secreted protien.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ss.
XX
OS Homo sapiens.
XX
PN WO9906554-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001238.
XX
PR 01-AUG-1997; 97US-00905134.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153784/13.
DR P-PSDB; AAY01594.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle
PT and heart tissue.
XX
PS Example 28; Page 160-161; 622pp; English.
XX
CC The present sequence represents a extended cDNA seqeunce derived from a
CC 5' EST encoding a secreted protien. The specification describes 5'
CC expressed sequence tags (ESTs, see AAX40826-X41093) for human secreted
CC proteins (see AAY01602 and AAY11994-Y12260). The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
            |||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
            |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
            ||||||||||||||| ||||||||||||||||||||||||
Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 222
AAX51777
ID   AAX51777 standard; cDNA; 848 BP.
XX
AC   AAX51777;
XX
DT   22-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' EST clone 58-35-2-F10-FL2.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906552-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB001236.
XX
PR   01-AUG-1997;   97US-00905223.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Lacroix B;
XX
DR   WPI; 1999-153782/13.
DR   P-PSDB; AAY12986.
XX
PT   New isolated brain-derived nucleic acids - used to develop products which
PT   may have cytokine, immune, regulatory, haematopoiesis regulating, anti-
PT   inflammatory or tumour inhibition activity.
XX
PS   Example 28; Page 159-160; 577pp; English.
XX
CC   AAX51787 to AAX52019 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY12987 to
CC   AAY13219, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell. This
CC   sequence represents the human secreted protein 5' EST clone 58-35-2-F10-
CC   FL2
XX
SQ   Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

  Query Match           98.0%;  Score 625;  DB 2;  Length 848;
  Best Local Similarity  99.2%;  Pred. No. 8.7e-181;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
            |||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
            |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 223
AAX51449
ID   AAX51449 standard; DNA; 848 BP.
XX
AC   AAX51449;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' BST SEQ ID NO. 27.
XX
KW   Human; secreted protein; BST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906549-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB001231.
XX
PR   01-AUG-1997;   97US-00905279.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Lacroix B;
XX
DR   WPI; 1999-153779/13.
DR   P-PSDB; AAY12679, AAY12680.
XX
PT   New nucleic acids encoding human secreted proteins - obtained from cDNA
PT   libraries derived from testis, ovary, uterus and spleen tissue.
XX
PS   Example 28; Page 159-160; 522pp; English.
XX
CC   AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY12681 to
CC   AAY12913, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell. This
CC   sequence represents an oligonucleotide used in an example in the
CC   invention, to the isolate the 5' EST sequences of the invention
XX
SQ   Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

  Query Match             98.0%;  Score 625;  DB 2;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 8.7e-181;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 224
AAX40428
ID   AAX40428 standard; cDNA; 848 BP.
XX
AC   AAX40428;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Extended cDNA derived from 5' EST.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906550-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB001232.
XX
PR   01-AUG-1997;   97US-00905144.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Lacroix B;
XX
DR   WPI; 1999-153780/13.
```

```
DR   P-PSDB; AAY11715.
XX
PT   New isolated prostate-derived nucleic acids - used to develop products
PT   which may have cytokine, immune regulatory, haematopoiesis regulating,
PT   anti-inflammatory or tumour inhibition activity.
XX
PS   Example 28; Page 160-161; 675pp; English.
XX
CC   AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins expressed in prostate, and encode the proteins
CC   given in AAY11716 to AAY11993 respectively. The proteins given represent
CC   the signal peptide and an N-terminal fragment of a secreted protein. The
CC   nucleic acid sequences can be used for producing secreted human gene
CC   products. They can also be used to develop products for diagnosis and
CC   therapy. The proteins obtained may have cytokine activity, cell
CC   proliferation and differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptides can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ   Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

  Query Match            98.0%;  Score 625;  DB 2;  Length 848;
  Best Local Similarity  99.2%;  Pred. No. 8.7e-181;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||| |||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 225
AAZ42251
ID   AAZ42251 standard; cDNA; 848 BP.
XX
AC   AAZ42251;
XX
DT   01-FEB-2000  (first entry)
XX
DE   Human full length cDNA 58-35-2-F10-FL2.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW   gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
KW   location; development; protein synthesis; stability; regulation;
KW   identification; ss.
XX
OS   Homo sapiens.
XX
PN   WO9953051-A2.
XX
PD   21-OCT-1999.
XX
PF   09-APR-1999;   99WO-IB000712.
XX
PR   09-APR-1998;   98US-00057719.
PR   28-APR-1998;   98US-00069047.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-038446/03.
DR   P-PSDB; AAY64646.
XX
PT   Novel secreted protein 5' expressed sequence tag sequences used in
PT   diagnostic, forensic, gene therapy, and chromosome mapping procedures.
XX
PS   Example 21; Page 167-168; 837pp; English.
XX
CC   AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC   sequences, corresponding to human secreted proteins. AAY64651 to AAY65438
CC   represent the EST-related proteins corresponding to AAZ42265 to AAZ43052.
CC   The 5' BSTs can be used for producing secreted human gene products. They
CC   can be used to identify and isolate 5' untranslated regions (UTRs) and
CC   upstream regulatory regions which control the location, development
CC   stage, rate, and quantity of protein synthesis, as well as stability of
CC   mRNA. The ESTs are also useful as probes for chromosome mapping, and to
CC   obtain full length cDNA clones. The ESTs can also be used in forensic
CC   procedures to identify individuals, or in diagnostic procedures to
CC   identify individuals having genetic diseases resulting from abnormal gene
CC   expression. The products may also be used in gene therapy protocols. The
CC   nucleic acids encoding signal peptides can be used for directing
CC   extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell. The
CC   proteins encoded by the EST sequences may be useful in treating a variety
CC   of human conditions. Secreted proteins have therapeutic value, and the
CC   identification of new secreted proteins is valuable. AAZ42249 to AAZ42264
CC   and AAY64644 to AAY64650 represent sequences used in the exemplification
CC   of the present invention
XX
SQ   Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

  Query Match            98.0%;  Score 625;  DB 3;  Length 848;
  Best Local Similarity  99.2%;  Pred. No. 8.7e-181;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91
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```
Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
             ||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||||
Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
             |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
             |||||||||||||| ||||||||||||||||||||||||
Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 226
AAC00012
ID   AAC00012 standard; cDNA; 848 BP.
XX
AC   AAC00012;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein cDNA sequence #3.
XX
KW   Human; secreted protein; 5' EST; expressed sequence tag; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             32. .700
FT                   /*tag=  a
FT                   /product= "secreted protein"
FT                   /transl_except= (pos:539. .541,aa:Xaa)
FT                   /transl_except= (pos:542. .544,aa:Xaa)
FT                   /transl_except= (pos:581. .583,aa:Xaa)
FT                   /transl_except= (pos:584. .586,aa:Xaa)
FT                   /note= "Xaa= unspecified amino acid"
FT   sig_peptide     32. .73
FT                   /*tag=  b
FT   mat_peptide     74. .697
FT                   /*tag=  c
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-00200610.
XX
PR   26-FEB-1999;   99US-0122487P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG00014, AAG00015.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS   Example 19; SEQ ID NO 5; 71pp + Sequence Listing; English.
XX
CC   The present sequence is a full length cDNA encoding a human secreted
CC   protein. The cDNA was obtained from a 5' EST using first and second
CC   strand synthesis procedures. 5' ESTs were prepared from total human RNAs
CC   or polyA+ RNAs derived from 30 different tissues. EST sequences usually
CC   correspond mainly to the 3' untranslated region (UTR) of the mRNA because
CC   they are often obtained from oligo-dT primed cDNA libraries. Such ESTs
CC   are not well suited for isolating cDNA sequences derived from the 5' ends
CC   of mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors
XX
SQ   Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

  Query Match             98.0%;  Score 625;  DB 3;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 8.7e-181;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;
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```
Qy         1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
             ||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||||
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```
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 227
AAX88191
ID AAX88191 standard; cDNA; 848 BP.
XX
AC AAX88191;
XX
DT 23-SEP-1999 (first entry)
XX
DE Human secreted protein 6 extended cDNA.
XX
KW Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
KW diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 32. .700
FT /*tag= a
FT /product= "secreted protein"
XX
PN WO9925825-A2.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-IB001862.
XX
PR 13-NOV-1997; 97US-0066677P.
PR 17-DEC-1997; 97US-0069957P.
PR 09-FEB-1998; 98US-0074121P.
PR 13-APR-1998; 98US-0081563P.
PR 10-AUG-1998; 98US-0096116P.
PR 04-SEP-1998; 98US-0099273P.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
DR WPI; 1999-347472/29.
DR P-PSDB; AAY25459, AAY25460.
XX
PT Extended cDNAs encoding secreted proteins.
XX
PS Example 28; Page 138; 307pp; English.
XX
CC This invention describes novel nucleic acid sequences of extended cDNAs
CC (see AAX97813-X97906) which encode human secreted proteins (see AAY36129-
CC Y36222) and which have cytostatic, thrombotic and osteopathic activity.
CC The extended cDNAs can be used to express secreted proteins or parts of
CC them or to obtain antibodies capable of binding to the secreted proteins.
CC They may also be used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. Uses also include design of expression
CC vectors and secretion vectors. This sequence represents an extended cDNA
CC sequence which encodes a secreted protein used in the method of the
CC invention
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 97.9%; Score 624.4; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.3e-180;
Matches 634; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||:|||| ||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAANTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 228
AAX30083
ID AAX30083 standard; cDNA; 847 BP.
XX
AC AAX30083;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO:27.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906548-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001222.
XX
PR 01-AUG-1997; 97US-00905135.
XX
PA (GEST) GENSET.
XX

PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153778/13.
DR P-PSDB; AAY04174.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
PT umbilical cord, placenta and colon tissue.
XX
PS Example 28; Page 174-175; 824pp; English.
XX
CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12261 to
CC AAY12514, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC present sequence represents a 5' EST from an example of the present
CC invention
XX
SQ Sequence 847 BP; 257 A; 178 C; 162 G; 244 T; 0 U; 6 Other;

Query Match 97.7%; Score 623.4; DB 2; Length 847;
Best Local Similarity 99.1%; Pred. No. 2.7e-180;
Matches 633; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 GCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 229
AAH98224/c
ID AAH98224 standard; cDNA; 1365 BP.
XX
AC AAH98224;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 81.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR P-PSDB; AAM23565.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 1; Page 234; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention
XX
SQ Sequence 1365 BP; 416 A; 244 C; 257 G; 448 T; 0 U; 0 Other;

Query Match 96.6%; Score 616; DB 4; Length 1365;
Best Local Similarity 99.7%; Pred. No. 6.2e-178;
Matches 638; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1335 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 1276

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1275 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 1216
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```
Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1215 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 1156

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1155 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 1096

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1095 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 1036

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1035 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 976

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       975 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 916

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       915 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 856

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       855 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 796

Qy       541 GACGCTGAAG-ATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       795 GACGCTGAAGAATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 736

Qy       600 CCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
            ||||||||||||||| |||||||||||||||||||||||
Db       735 CCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 696
```

RESULT 230
AAX97957
ID AAX97957 standard; DNA; 1356 BP.
XX
AC AAX97957;
XX
DT 17-SEP-1999 (first entry)
XX
DE Human secreted protein gene 42.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO9931117-A1.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-US027059.
XX
PR 18-DEC-1997; 97US-0068006P.
PR 18-DEC-1997; 97US-0068007P.
PR 18-DEC-1997; 97US-0068008P.
PR 18-DEC-1997; 97US-0068053P.
PR 18-DEC-1997; 97US-0068054P.
PR 18-DEC-1997; 97US-0068057P.
PR 18-DEC-1997; 97US-0068064P.
PR 18-DEC-1997; 97US-0070923P.
PR 19-DEC-1997; 97US-0068169P.
PR 19-DEC-1997; 97US-0068365P.
PR 19-DEC-1997; 97US-0068367P.
PR 19-DEC-1997; 97US-0068368P.
PR 19-DEC-1997; 97US-0068369P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence K, Duan RD, Florence C, Greene JM, Feng P;
PI Ferrie AM, Yu G, Janat F, Ni J;
XX
DR WPI; 1999-418749/35.
DR P-PSDB; AAY36265.
XX
PT New isolated human genes encoding secreted polypeptides.
XX
PS Claim 1; Page 296-297; 537pp; English.
XX
CC AAX97916 to AAX98029 represent 110 isolated human secreted protein genes.
CC AAY36224 to AAY36727 represent the secreted proteins encoded by the 110
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 110 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences given
CC in AAX97907 to AAX97915 and AAY36223 are used in the exemplification of
CC the present invention
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 96.4%; Score 615; DB 2; Length 1356;
Best Local Similarity 99.7%; Pred. No. 1.3e-177;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy         1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        18 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 77

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        78 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 137

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       138 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 197

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       198 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGA-G 256

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       257 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 316

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       317 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 376

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       377 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 436

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       437 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 496
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```
Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 556

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 616

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||||||||||||||||||||||||
Db        617 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 655
```

RESULT 231
ADA56545
ID ADA56545 standard; DNA; 1356 BP.
XX
AC ADA56545;
XX
DT 20-NOV-2003 (first entry)
XX
DE Gene encoding human secreted protein #269.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR P-PSDB; ADA57438.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 21; SEQ ID NO 734; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 96.4%; Score 615; DB 7; Length 1356;
Best Local Similarity 99.7%; Pred. No. 1.3e-177;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 77

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 137

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 197

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        198 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGA-G 256

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 316

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 376

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 436

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 496

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 556

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 616

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||||||||||||||||||||||||
Db        617 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 655
```

RESULT 232
ADA40381
ID ADA40381 standard; cDNA; 1356 BP.
XX
AC ADA40381;

XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 9; SEQ ID NO 763; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 96.4%; Score 615; DB 7; Length 1356;
Best Local Similarity 99.7%; Pred. No. 1.3e-177;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         18 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 77

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         78 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 137

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        138 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 197

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        317 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 376

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        377 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 436

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        437 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 496

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        557 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 616

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
                |||||||||||||| ||||||||||||||||||||||||
Db        617 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 655
```

RESULT 233
ADA11594
ID ADA11594 standard; DNA; 1356 BP.
XX
AC ADA11594;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.
XX
KW cancer; inflammation; immune disorder; neurological disorder;
KW blood clotting disorder; food additive; food preservative;
KW storage capability; fat content; nutritional component; ds; gene; human.
XX
OS Homo sapiens.
XX
PN US2003055236-A1.
XX
PD 20-MAR-2003.
XX
PF 14-MAR-2002; 2002US-00097065.
XX
PR 18-DEC-1997; 97US-0068006P.
PR 18-DEC-1997; 97US-0068007P.
PR 18-DEC-1997; 97US-0068008P.
PR 18-DEC-1997; 97US-0068053P.
PR 18-DEC-1997; 97US-0068054P.
PR 18-DEC-1997; 97US-0068057P.
PR 18-DEC-1997; 97US-0068064P.

PR 18-DEC-1997; 97US-0070923P.
PR 19-DEC-1997; 97US-0068169P.
PR 19-DEC-1997; 97US-0068365P.
PR 19-DEC-1997; 97US-0068367P.
PR 19-DEC-1997; 97US-0068368P.
PR 19-DEC-1997; 97US-0068369P.
PR 17-DEC-1998; 98WO-US027059.
PR 17-JUN-1999; 99US-00334595.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence KA, Duan DR, Florence C, Greene JM, Feng P;
PI Perrie AM, Yu G, Janat F, Ni J;
XX
DR WPI; 2003-567105/53.
DR P-PSDB; ADA11718.
XX
PT New secreted HKABT24 nucleic acid molecules and polypeptides, useful for
PT preventing, treating, or ameliorating a medical condition, such as
PT cancer, inflammation, immune disorders, neurological and blood clotting
PT disorders.
XX
PS Claim 1; SEQ ID NO 122; 118pp; English.
XX
CC The invention relates to an isolated HKABT24 nucleic acid molecule. The
CC polypeptides, nucleic acids and antibodies are useful for diagnosing a
CC pathological condition or a susceptibility to a pathological condition,
CC for preventing, treating, or ameliorating a medical condition, such as
CC cancer, inflammation and other immune disorders, neurological and blood
CC clotting disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
CC antagonist may also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content or other
CC nutritional components. The present sequence represents cDNA encoding a
CC novel human secreted protein. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 96.4%; Score 615; DB 8; Length 1356;
Best Local Similarity 99.7%; Pred. No. 1.3e-177;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 77

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         78 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 137

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 197

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        198 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGA-G 256

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        317 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 376

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        437 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 496

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        617 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 655
```

RESULT 234
ADD37752
ID ADD37752 standard; cDNA; 1356 BP.
XX
AC ADD37752;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted protein encoding sequence #234.
XX
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US008279.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-140218/13.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or asthmatic disorders, or related immediate
PT hypersensitivity disorders.
XX
PS Claim 7; SEQ ID NO 234; 1323pp; English.
XX
CC The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or asthmatic disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases , wound healing and disorders of epithelial cell
CC proliferation, immune disorders , cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders , or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome

CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein encoding sequence.
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 96.4%; Score 615; DB 9; Length 1356;
Best Local Similarity 99.7%; Pred. No. 1.3e-177;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         18 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 77

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 137

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        257 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 316

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        317 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 376

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        377 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 436

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        497 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 556

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Job time : 283.223 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 09:17:55 ; Search time 2500.23 Seconds
(without alignments)
11060.139 Million cell updates/sec

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Perfect score: 638
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

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6: gb_pat:*
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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	638	100.0	1346	6	AX464348	AX464348 Sequence
4	638	100.0	1346	9	AY359060	AY359060 Homo sapi
5	627	98.3	666	6	AX083382	AX083382 Sequence
6	627	98.3	1347	6	AX083392	AX083392 Sequence
7	627	98.3	1377	9	BC050606	BC050606 Homo sapi
8	627	98.3	1440	9	BC015099	BC015099 Homo sapi
9	627	98.3	1605	9	BC014317	BC014317 Homo sapi
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11	625.4	98.0	1345	9	AF229179	AF229179 Homo sapi
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15	625	98.0	848	6	AR340701	AR340701 Sequence
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23	625	98.0	848	6	BD077436	BD077436 5'EST of
24	625	98.0	848	6	BD077737	BD077737 5'EST of
25	625	98.0	848	6	BD085880	BD085880 Elongatio
26	625	98.0	848	6	BD107926	BD107926 EST and e
27	625	98.0	848	6	BD131408	BD131408 cDNA enco
28	625	98.0	848	6	BD139270	BD139270 Extended
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30	615	96.4	1356	6	BD135300	BD135300 110 human

ALIGNMENTS

RESULT 1
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LOCUS AR252633 1346 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 386 from patent US 6478825.
ACCESSION AR252633
VERSION AR252633.1 GI:27300541
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 386 12-NOV-2002;
FEATURES Location/Qualifiers
source 1. .1346
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 638; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.4e-165;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
Db 7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy 61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

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Db        67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db       127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db       187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db       247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db       307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db       367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db       427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

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Qy       601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638

Db       607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644
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RESULT 2
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LOCUS AX403499 1346 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 386 from Patent WO0073454.
ACCESSION AX403499
VERSION AX403499.1 GI:21436987
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 386 07-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 638; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.4e-165;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

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Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db       127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db       187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db       247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db       307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db       367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

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Db       547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy       601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638

Db       607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644
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RESULT 3
AX464348
LOCUS AX464348 1346 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 481 07-JUN-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 638; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.4e-165;

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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638
              |||||||||||||||||||||||||||||||||||||
Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644


RESULT 4
AY359060
LOCUS       AY359060                1346 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION   AY359060
VERSION     AY359060.1  GI:37183237
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309

REFERENCE   2  (bases 1 to 1346)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="Homo sapiens"
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     gene            1. .1346
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     CDS             7. .645
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                     /note="PRO1312"
                     /codon_start=1
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                     /protein_id="AAQ89419.1"
                     /db_xref="GI:37183238"
                     /translation="MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDT
                     NEEYLFKAMVAFSMRKVPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQ
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGILMMPS"
ORIGIN

  Query Match             100.0%;  Score 638;  DB 9;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-165;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638
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RESULT 5
AX083382
LOCUS       AX083382                 666 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 74 from Patent WO0112660.
ACCESSION   AX083382
VERSION     AX083382.1  GI:13185219
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 74 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             98.3%;  Score 627;  DB 6;  Length 666;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-162;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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RESULT 6
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LOCUS       AX083392                1347 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 84 from Patent WO0112660.
ACCESSION   AX083392
VERSION     AX083392.1  GI:13185232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 84 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /codon_start=1
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                     /db_xref="GI:13185233"
                     /db_xref="REMTREMBL:CAC33295"
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                     LTPL"
ORIGIN

  Query Match             98.3%;  Score 627;  DB 6;  Length 1347;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-162;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 85

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         86 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 145

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        146 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 205

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        206 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 265

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        266 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 325

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db        626 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 664
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RESULT 7
BC050606
LOCUS BC050606 1377 bp mRNA linear PRI 12-NOV-2003
DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone MGC:60059 IMAGE:5183554), complete cds.
ACCESSION BC050606
VERSION BC050606.1 GI:30047080
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1377)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1377)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 110 Row: c Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361864.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 98.3%; Score 627; DB 9; Length 1377;
Best Local Similarity 99.8%; Pred. No. 2.6e-162;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 8
BC015099
LOCUS       BC015099               1440 bp    mRNA    linear   PRI 04-OCT-2003
DEFINITION  Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
            MGC:22827 IMAGE:3829035), complete cds.
ACCESSION   BC015099
VERSION     BC015099.1  GI:15929328
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1440)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                     LTPL"
ORIGIN

  Query Match             98.3%;  Score 627;  DB 9;  Length 1440;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-162;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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RESULT 9
BC014317
LOCUS       BC014317               1605 bp    mRNA    linear   PRI 04-OCT-2003
DEFINITION  Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
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ACCESSION   BC014317
VERSION     BC014317.1  GI:15680012
KEYWORDS    MGC.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1605)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1605)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 31 Row: n Column: 3.
FEATURES Location/Qualifiers
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/tissue_type="Bone marrow, chronic myelogenous leukemia"
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/lab_host="DH10B"
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LTPL"
ORIGIN

Query Match 98.3%; Score 627; DB 9; Length 1605;
Best Local Similarity 99.8%; Pred. No. 2.6e-162;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db        801 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 860

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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RESULT 10
BD205644
LOCUS BD205644 1447 bp DNA linear PAT 17-JUL-2003
DEFINITION 97 human secreted proteins.
ACCESSION BD205644
VERSION BD205644.1 GI:33015414
KEYWORDS JP 2002533058-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1447)
AUTHORS Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C., Moore,P.A., Olsen,H.S., Shi,Y., Young,P.B., Wei,F.F., Brewer,L.A., Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
TITLE 97 human secreted proteins
JOURNAL Patent: JP 2002533058-A 21 08-OCT-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002533058-A/21

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            PD   08-OCT-2002
            PF   06-MAY-1999 JP 2000548451
            PR   12-MAY-1998 US    60/085093,12-MAY-1998 US    60/085094 PR
            12-MAY-1998 US    60/085105,12-MAY-1998 US    60/085180 PR
            18-MAY-1998 US    60/085927,18-MAY-1998 US    60/085906 PR
            18-MAY-1998 US    60/085924,18-MAY-1998 US    60/085922 PR
            18-MAY-1998 US    60/085923,18-MAY-1998 US    60/085921 PR
            18-MAY-1998 US    60/085925,18-MAY-1998 US    60/085928 PR
            18-MAY-1998 US    60/085920
            PI   STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH

            PI   C CARTER,
            PI   PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI
            PI   WEI,
            PI   LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A  PI
             ENDRESS,
            PI   REINHARD EBNER
            PC   C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12P21/02,C12N15/00,C12N5/00
            CC   97 human secreted proteins.
            FH   Key             Location/Qualifiers
            FT   source          1. .1447
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1447
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.2%;  Score 626.6;  DB 6;  Length 1447;
  Best Local Similarity   99.7%;  Pred. No. 3.3e-162;
  Matches  637;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 136

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        497 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 556

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db        677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 715


RESULT 11
AF229179
LOCUS       AF229179                1345 bp    mRNA    linear   PRI 05-APR-2002
DEFINITION  Homo sapiens collectrin mRNA, complete cds.
ACCESSION   AF229179
VERSION     AF229179.1  GI:9957753
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K.,
            Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.
  TITLE     Collectrin, a collecting duct-specific transmembrane glycoprotein,
            is a novel homolog of ACE2 and is developmentally regulated in
            embryonic kidneys
  JOURNAL   J. Biol. Chem. 276 (20), 17132-17139 (2001)
  MEDLINE   21264468
   PUBMED   11278314
REFERENCE   2  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Human kidney specific membrane protein (NX-17)
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-2000) Department of Medicine III, Okayama
            University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,
            Japan
FEATURES             Location/Qualifiers
     source          1. .1345
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             24. .692
                     /note="kidney-specific membrane protein NX-17; similar to
                     the Mus musculus and Rattus norvegicus products encoded by
                     GenBank Accession Numbers AF178085 and AF178086,
                     respectively"
                     /codon_start=1
                     /product="collectrin"
                     /protein_id="AAG09466.1"
                     /db_xref="GI:9957754"
                     /translation="MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDT
                     NEEYLFKAMVAFSMRKVPNREATEISHVLLCNVTQRVSPWFVVTDPSKNHTLPAVEVQ
                     SAIRMNKNRINNAFFLNDQTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL
                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                     LTPL"
ORIGIN

  Query Match             98.0%;  Score 625.4;  DB 9;  Length 1345;
  Best Local Similarity   99.7%;  Pred. No. 7.2e-162;
  Matches  637;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 83

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 143

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 203
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 263

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAA 323

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 383

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 443

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 503

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 563

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 623

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db        624 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 662
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RESULT 12
BD083420

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LOCUS       BD083420                1401 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD083420
VERSION     BD083420.1  GI:22629030
KEYWORDS    JP 2001523950-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1401)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2001523950-A 2 27-NOV-2001;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2001523950-A/2
            PD   27-NOV-2001
            PF   23-JAN-1998 JP 1998532177
            PR   24-JAN-1997 US     08/788789
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1401
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                        /db_xref="taxon:32630"
ORIGIN

  Query Match             98.0%;  Score 625.4;  DB 6;  Length 1401;
  Best Local Similarity   99.7%;  Pred. No. 7.2e-162;
  Matches  637;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         71 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 130
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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 190

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 250

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 310

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        311 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 370

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        371 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTAAATGAC 430

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 490

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 550

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        551 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 610

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        611 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 670

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db        671 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 709
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RESULT 13
AR177334

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LOCUS       AR177334                  848 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 27 from patent US 6312922.
ACCESSION   AR177334
VERSION     AR177334.1  GI:17919689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
  TITLE     Complementary DNAs
  JOURNAL   Patent: US 6312922-A 27 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638

Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 14
BD247957
LOCUS BD247957 848 bp DNA linear PAT 17-JUL-2003
DEFINITION 5' ESTs for secreted proteins expressed in various tissues.
ACCESSION BD247957
VERSION BD247957.1 GI:33057727
KEYWORDS JP 2002525024-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: JP 2002525024-A 22 13-AUG-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002525024-A/22
PD 13-AUG-2002
PF 31-JUL-1998 JP 2000505294
PR 01-AUG-1997 US 08/905051
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12M1/00,C12P21/02,C12N15/00, PC
C12N15/00
CC Von Heijne matrix
CC score 10.7
CC seq LWLLPFLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32. .73.
FEATURES Location/Qualifiers
source 1. .848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy         1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db        32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db       572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638

Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
```

RESULT 15
AR340701
LOCUS AR340701 848 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 27 from patent US 6573068.
ACCESSION AR340701
VERSION AR340701.1 GI:33732443
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 848)
AUTHORS Milne Edwards,J.-B.D., Duclert,A. and Bougueleret,L.
TITLE Claudin-50 protein
JOURNAL Patent: US 6573068-A 27 03-JUN-2003;
FEATURES Location/Qualifiers
source 1. .848
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

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  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 16
AR412373
LOCUS       AR412373                 848 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6639063.
ACCESSION   AR412373
VERSION     AR412373.1  GI:40167483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE     EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 5 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;
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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 17
AX884142
LOCUS       AX884142                 848 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from Patent EP1033401.
ACCESSION   AX884142
VERSION     AX884142.1  GI:40039026
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
  TITLE     Expressed sequence tags and encoded human proteins
  JOURNAL   Patent: EP 1033401-A 5 06-SEP-2000;
            Genset (FR)
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             32. .700
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAE93778.1"
                     /db_xref="GI:40039027"
                     /translation="MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDT
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                    SAIRMNKNRINNAFFLNDQTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL
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                    LTPL"
     sig_peptide    32. .73
                    /note="Von Heijne matrix"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 18
BD023757
LOCUS       BD023757                848 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD023757
VERSION     BD023757.1  GI:22564980
KEYWORDS    JP 2001269182-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 3 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/3
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
              G06F15/40
            CC   Von Heijne matrix
            FH   Key             Location/Qualifiers
            FT   CDS             32. .697
            FT   sig_peptide     32. .73.
FEATURES                Location/Qualifiers
     source             1. .848
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 19
BD073618
LOCUS       BD073618                848 bp    DNA     linear   PAT 27-AUG-2002
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DEFINITION  5'EST of secreted protein expressing in testis and other tissues.
ACCESSION   BD073618
VERSION     BD073618.1  GI:22619221
KEYWORDS    JP 2001512012-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Baputist,D.M.E.J., Eimeric,D. and Bruno,L.
  TITLE     5'EST of secreted protein expressing in testis and other tissues
  JOURNAL   Patent: JP 2001512012-A 22 21-AUG-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001512012-A/22
            PD   21-AUG-2001
            PF   31-JUL-1998 JP 2000505290
            PR   01-AUG-1997 US     08/905279
            PI   DUMAS MILNE EDWARDS JEAN BAPUTIST,DUCLAIR EIMERIC,LACROIX  PI
             BRUNO
            PC   C12N15/09,A61K38/00,A61K48/00,C07K14/435,C07K19/00,C12P21/02,
            PC   C12Q1/68,
            PC   G01N33/50,G01N33/53,G01N33/53,G01N33/566,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   score 10.7
            CC   seq LWLLFFLVTAIHA/EL
            FH   Key             Location/Qualifiers
            FT   sig_peptide     32. .73.
FEATURES             Location/Qualifiers
     source          1. .848
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 20
BD075896
LOCUS       BD075896                 848 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  5' EST of secretory protein expressed in endoblast.
ACCESSION   BD075896
VERSION     BD075896.1  GI:22621499
KEYWORDS    JP 2001512005-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
  TITLE     5' EST of secretory protein expressed in endoblast
  JOURNAL   Patent: JP 2001512005-A 22 21-AUG-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001512005-A/22
            PD   21-AUG-2001
            PF   31-JUL-1998 JP 2000505194
            PR   01-AUG-1997 US     08/904468
            PI   JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO  PI
            LACROIX
            PC   C12N15/09,C07K19/00,C12M1/00,C12N1/15,C12N1/19,C12N1/21,C12N5/
            PC   10,C12Q1/68,
            PC   C12N15/00,C12N5/00
            CC   Von Heijne matrix
            CC   score 10.7
            CC   seq LWLLFFLVTAIHA/EL
            FH   Key             Location/Qualifiers
            FT   sig_peptide     32. .73.
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 21
BD076074
LOCUS BD076074 848 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076074
VERSION BD076074.1 GI:22621677
KEYWORDS JP 2001512011-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 22 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/22
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
Von Heijne matrix
CC score 10.7
CC seq LWLLPFLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32. .73.
FEATURES Location/Qualifiers
source 1. .848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151
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Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 22
BD076775
LOCUS BD076775 848 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of secretory protein expressed in prostate.
ACCESSION BD076775
VERSION BD076775.1 GI:22622378
KEYWORDS JP 2001512013-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of secretory protein expressed in prostate
JOURNAL Patent: JP 2001512013-A 22 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512013-A/22
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/02,C12Q1/68,C12N15/00 CC
Von Heijne matrix
CC score 10.7
CC seq LWLLPFLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32. .73.
FEATURES Location/Qualifiers
source 1. .848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

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  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 23
BD077436
LOCUS       BD077436                 848 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  5'EST of secreted protein expressed in muscles and other mesodermal
            tissues.
ACCESSION   BD077436
VERSION     BD077436.1  GI:22623039
KEYWORDS    JP 2001512016-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
  TITLE     5'EST of secreted protein expressed in muscles and other mesodermal
            tissues
  JOURNAL   Patent: JP 2001512016-A 22 21-AUG-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001512016-A/22
            PD   21-AUG-2001
            PF   31-JUL-1998 JP 2000505295
            PR   01-AUG-1997 US    08/905134
            PI   JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO  PI
            LACROIX
            PC   C12N15/09,C12N15/09,C07K14/47,C12M1/00,C12N15/00,C12N15/00 CC
             Von Heijne matrix
            CC   score 10.7
            CC   seq LWLLPFLVTAIHA/EL
            FH   Key             Location/Qualifiers
            FT   sig_peptide     32. .73.
FEATURES              Location/Qualifiers
     source           1. .848
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN
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  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 24
BD077737
LOCUS       BD077737                 848 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  5'EST of secretory protein in brain.
ACCESSION   BD077737
VERSION     BD077737.1  GI:22623340
KEYWORDS    JP 2001512015-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
  TITLE     5'EST of secretory protein in brain
  JOURNAL   Patent: JP 2001512015-A 22 21-AUG-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001512015-A/22
            PD   21-AUG-2001
            PF   31-JUL-1998 JP 2000505293
            PR   01-AUG-1997 US    08/905223
            PI   JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO  PI
            LACROIX
            PC   C12N15/09,C07K14/47,C12M1/00,C12P21/02,C12Q1/68,C12N15/00 CC
            Von Heijne matrix
            CC   score 10.7
            CC   seq LWLLPFLVTAIHA/EL
            FH   Key             Location/Qualifiers
            FT   sig_peptide     32. .73.
FEATURES            Location/Qualifiers
     source         1. .848
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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Db         632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670


RESULT 25
BD085880
LOCUS       BD085880                 848 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Elongation cDNA of secretory protein.
ACCESSION   BD085880
VERSION     BD085880.1  GI:22631490
KEYWORDS    JP 2001523453-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
  TITLE     Elongation cDNA of secretory protein
  JOURNAL   Patent: JP 2001523453-A 22 27-NOV-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001523453-A/22
            PD   27-NOV-2001
            PF   13-NOV-1998 JP 2000521191
            PR   13-NOV-1997 US    60/066677,17-DEC-1997 US    60/069957 PR
            09-FEB-1998 US    60/074121,13-APR-1998 US    60/081563 PR
            10-AUG-1998 US    60/096116,04-SEP-1998 US    60/099273 PI   LYDIE
            BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE  PI   EDWARDS
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
            Von Heijne matrix
            FH   Key             Location/Qualifiers
            FT   sig_peptide     32. .73.
FEATURES            Location/Qualifiers
     source         1. .848
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638

Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 26
BD107926
LOCUS BD107926 848 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD107926
VERSION BD107926.1 GI:23202744
KEYWORDS JP 2002010789-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 3 15-JAN-2002;
GENSET CORP
COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/3
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE PI
GIORDANO
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
C12N15/00
CC Von Heijne matrix
FH Key Location/Qualifiers
FT CDS 32. .697
FT sig_peptide 32. .73.
FEATURES Location/Qualifiers
source 1. .848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638

Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 27
BD131408
LOCUS BD131408 848 bp DNA linear PAT 18-SEP-2002
DEFINITION cDNA encoding secretory protein.
ACCESSION BD131408
VERSION BD131408.1 GI:23226353
KEYWORDS JP 2002502605-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE cDNA encoding secretory protein
JOURNAL Patent: JP 2002502605-A 22 29-JAN-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002502605-A/22
PD 29-JAN-2002
PF 09-FEB-1999 JP 2000530603
PR 09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PI LYDIE
BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12M1/00,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68//G06F17/30,C12N15/00, PC
C12N5/00,
PC C12N15/00
CC Von Heijne matrix
FH Key Location/Qualifiers
FT sig_peptide 32. .73.
FEATURES Location/Qualifiers
source 1. .848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db        32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy        61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db        92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy       121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db       152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy       181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db       212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy       241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db       272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy       301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db       332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy       361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db       392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy       421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db       452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy       481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db       512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy       541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db       572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy       601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638

Db       632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 28
BD139270

LOCUS	BD139270 848 bp DNA linear PAT 18-SEP-2002
DEFINITION	Extended cDNA of secretory protein.
ACCESSION	BD139270
VERSION	BD139270.1 GI:23234215
KEYWORDS	JP 2002508182-A/22.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 848)
AUTHORS	Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE	Extended cDNA of secretory protein
JOURNAL	Patent: JP 2002508182-A 22 19-MAR-2002;
	GENSET
COMMENT	OS Homo sapiens (human)
	PN JP 2002508182-A/22
	PD 19-MAR-2002
	PF 17-DEC-1998 JP 2000539136
	PR 17-DEC-1997 US 60/069957,09-FEB-1998 US 60/074121 PR
	13-APR-1998 US 60/081563,10-AUG-1998 US 60/096116 PI LYDIE
	BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
	PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
	C12N1/21,
	PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
	Von Heijne matrix
	FH Key Location/Qualifiers
	FT sig_peptide 32. .73.

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FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638

Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 29
BD203799

LOCUS	BD203799 848 bp DNA linear PAT 17-JUL-2003
DEFINITION	5'EST and human protein encoded thereby.
ACCESSION	BD203799
VERSION	BD203799.1 GI:33013569
KEYWORDS	JP 2002511259-A/3.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 848)
AUTHORS	Edwards,J.B.D.M., Duclert,A. and Giordano,J.Y.
TITLE	5'EST and human protein encoded thereby
JOURNAL	Patent: JP 2002511259-A 3 16-APR-2002;
	GENSET
COMMENT	OS Homo sapiens (human)

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            PN   JP 2002511259-A/3
            PD   16-APR-2002
            PF   09-APR-1999 JP 2000543599
            PR   09-APR-1998 US    09/057719,28-APR-1998 US    09/069047 PI
            JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,JEAN YVES  PI
            GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12M1/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/566, PC
             G06F17/50//
            PC   G06F17/30,C12N15/00,C12N5/00,C12N15/00
            CC   Von Heijne matrix
            FH   Key             Location/Qualifiers
            FT   CDS             32. .697
            FT   sig_peptide     32. .73.
FEATURES                Location/Qualifiers
     source             1. .848
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
ORIGIN

  Query Match             98.0%;  Score 625;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9.3e-162;
  Matches  634;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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RESULT 30
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ACCESSION   BD135300
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  AUTHORS   Moore,P.A., Ruben,S.M., Carter,K.C., Shi,Y., Rosen,C.A.,
            Soppet,D.R., Caou,H., Wei,Y.F., Florence,K., Duan,R.D.,
            Florence,C., Greene,J.M., Feng,P., Ferrie,A.M., Yu,G.L., Janat,F.
            and Ni,J.
  TITLE     110 human secretory proteins
  JOURNAL   Patent: JP 2002508167-A 51 19-MAR-2002;
            HUMAN GENOME SCIENCES INC
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            19-DEC-1997 US   60/068 365
            PI   PAUL A MOORE,STEVEN M RUBEN,KENNETH C CARTER,YANGGU SHI,CRAIG
            PI   A ROSEN,
            PI   DANIEL R SOPPET,HARA CAOU,YING FEI WEI,KIMBERLY FLORENCE, PI
            ROSANNE D DUAN,
            PI   CHARLES FLORENCE,JOHN M GREENE,PING FENG,ANN M FERRIE,GUO  PI
             LIANG YU,
            PI   FORD JANAT,JIAN NI
            PC   C12N15/09,A61K38/00,A61K48/00,A61P9/00,A61P9/10,A61P15/00, PC
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Search completed: June  6, 2004, 13:05:23
Job time : 2507.23 secs
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 13:05:30 ; Search time 273.337 Seconds
(without alignments)
10648.235 Million cell updates/sec

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Perfect score: 638
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 518

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Post-processing: Minimum Match 80%
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Listing first 65000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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441	638	100.0	1346	15	US-10-123-212-481	Sequence 481, App
442	638	100.0	1346	15	US-10-123-213-481	Sequence 481, App
443	638	100.0	1346	15	US-10-123-291-481	Sequence 481, App
444	638	100.0	1346	15	US-10-123-322-481	Sequence 481, App
445	638	100.0	1346	15	US-10-123-771-481	Sequence 481, App
446	638	100.0	1346	15	US-10-123-911-481	Sequence 481, App
447	638	100.0	1346	15	US-10-124-823-481	Sequence 481, App
448	638	100.0	1346	15	US-10-125-931-481	Sequence 481, App
449	638	100.0	1346	15	US-10-125-932-481	Sequence 481, App
450	638	100.0	1346	16	US-10-123-913-481	Sequence 481, App
451	638	100.0	1346	16	US-10-137-867-481	Sequence 481, App
452	638	100.0	1346	16	US-10-140-473-481	Sequence 481, App
453	638	100.0	1346	16	US-10-140-806-481	Sequence 481, App
454	638	100.0	1346	16	US-10-140-810-481	Sequence 481, App
455	638	100.0	1346	16	US-10-140-863-481	Sequence 481, App
456	638	100.0	1346	16	US-10-141-699-481	Sequence 481, App
457	638	100.0	1346	16	US-10-141-703-481	Sequence 481, App
458	638	100.0	1346	16	US-10-141-706-481	Sequence 481, App
459	638	100.0	1346	16	US-10-141-757-481	Sequence 481, App
460	638	100.0	1346	16	US-10-141-762-481	Sequence 481, App
461	638	100.0	1346	16	US-10-142-428-481	Sequence 481, App
462	638	100.0	1346	16	US-10-142-429-481	Sequence 481, App
463	638	100.0	1346	16	US-10-142-884-481	Sequence 481, App
464	638	100.0	1346	16	US-10-143-027-481	Sequence 481, App
465	638	100.0	1346	16	US-10-143-115-481	Sequence 481, App
466	638	100.0	1346	16	US-10-144-956-481	Sequence 481, App
467	638	100.0	1346	16	US-10-144-958-481	Sequence 481, App
468	638	100.0	1346	16	US-10-145-632-481	Sequence 481, App
469	638	100.0	1346	16	US-10-145-749-481	Sequence 481, App
470	638	100.0	1346	16	US-10-145-753-481	Sequence 481, App
471	638	100.0	1346	16	US-10-145-871-481	Sequence 481, App
472	638	100.0	1346	16	US-10-145-878-481	Sequence 481, App
473	638	100.0	1346	16	US-10-146-794-481	Sequence 481, App
474	638	100.0	1346	16	US-10-147-489-481	Sequence 481, App
475	638	100.0	1346	16	US-10-147-507-481	Sequence 481, App
476	638	100.0	1346	16	US-10-147-535-481	Sequence 481, App
477	638	100.0	1346	16	US-10-147-537-481	Sequence 481, App
478	638	100.0	1346	16	US-10-152-376-481	Sequence 481, App
479	638	100.0	1346	16	US-10-152-381-481	Sequence 481, App
480	638	100.0	1346	16	US-10-152-400-481	Sequence 481, App
481	638	100.0	1346	16	US-10-153-585-481	Sequence 481, App
482	638	100.0	1346	16	US-10-157-780-481	Sequence 481, App
483	638	100.0	1346	16	US-10-157-800-481	Sequence 481, App
484	638	100.0	1346	16	US-10-157-801-481	Sequence 481, App
485	638	100.0	1346	16	US-10-157-802-481	Sequence 481, App
486	638	100.0	1346	16	US-10-158-784-481	Sequence 481, App
487	638	100.0	1346	16	US-10-158-789-481	Sequence 481, App
488	638	100.0	1346	16	US-10-192-011-481	Sequence 481, App
489	638	100.0	1346	16	US-10-139-963-481	Sequence 481, App
490	638	100.0	1346	16	US-10-140-020-481	Sequence 481, App
491	638	100.0	1346	16	US-10-140-023-481	Sequence 481, App
492	638	100.0	1346	16	US-10-140-809-481	Sequence 481, App
493	638	100.0	1346	16	US-10-140-865-481	Sequence 481, App
494	638	100.0	1346	16	US-10-141-701-481	Sequence 481, App
495	638	100.0	1346	16	US-10-141-754-481	Sequence 481, App
496	638	100.0	1346	16	US-10-141-760-481	Sequence 481, App
497	638	100.0	1346	16	US-10-142-425-481	Sequence 481, App
498	638	100.0	1346	16	US-10-142-430-481	Sequence 481, App
499	638	100.0	1346	16	US-10-143-113-481	Sequence 481, App
500	638	100.0	1346	16	US-10-146-730-481	Sequence 481, App
501	638	100.0	1346	16	US-10-146-792-481	Sequence 481, App
502	638	100.0	1346	16	US-10-158-791-481	Sequence 481, App
503	638	100.0	1346	16	US-10-156-843-481	Sequence 481, App
504	638	100.0	1346	16	US-10-157-786-481	Sequence 481, App
505	638	100.0	1346	16	US-10-219-538-386	Sequence 386, App
506	638	100.0	1346	16	US-10-147-528-481	Sequence 481, App
507	638	100.0	1346	16	US-10-128-692A-481	Sequence 481, App
508	638	100.0	1346	16	US-10-140-927-481	Sequence 481, App
509	638	100.0	1346	17	US-10-147-536-481	Sequence 481, App
510	627	98.3	1312	15	US-10-133-013-205	Sequence 205, App
511	627	98.3	1432	13	US-10-372-876-17	Sequence 17, Appl
512	627	98.3	1432	15	US-10-097-065-17	Sequence 17, Appl
513	626.6	98.2	1447	10	US-09-892-877-22	Sequence 22, Appl
514	626.6	98.2	1447	10	US-09-948-783-22	Sequence 22, Appl
515	625	98.0	848	10	US-09-903-190-27	Sequence 27, Appl
516	625	98.0	848	15	US-10-319-763-27	Sequence 27, Appl
517	615	96.4	1356	13	US-10-372-876-122	Sequence 122, App
518	615	96.4	1356	15	US-10-097-065-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-09-989-722-386

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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638

Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644


RESULT 508
US-10-140-927-481
; Sequence 481, Application US/10140927
; Publication No. US20040009548A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C180
;  CURRENT APPLICATION NUMBER: US/10/140,927
;  CURRENT FILING DATE:  2002-05-07
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
;   LENGTH: 1346
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-927-481

  Query Match             100.0%;  Score 638;  DB 16;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-186;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638

Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644


RESULT 509
US-10-147-536-481
; Sequence 481, Application US/10147536
; Publication No. US20040077064A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C349
;  CURRENT APPLICATION NUMBER: US/10/147,536
;  CURRENT FILING DATE:  2002-05-17
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
;   LENGTH: 1346
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-147-536-481

  Query Match             100.0%;  Score 638;  DB 17;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-186;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638
              |||||||||||||||||||||||||||||||||||||
Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644
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RESULT 510
US-10-133-013-205
; Sequence 205, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 205
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 2580580cB1
US-10-133-013-205

Query Match 98.3%; Score 627; DB 15; Length 1312;
Best Local Similarity 99.8%; Pred. No. 7.2e-183;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 68

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 128

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        129 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 188

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 248

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 308

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 368

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 428

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 488

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 548

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 608

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        609 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 647
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RESULT 511
US-10-372-876-17
; Sequence 17, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-372-876-17

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  Query Match             98.3%;  Score 627;  DB 13;  Length 1432;
  Best Local Similarity   99.8%;  Pred. No. 7.6e-183;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 128

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 188

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 248

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 308

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 368

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 428

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 488

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 548

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 608

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 668

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        669 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 707


RESULT 512
US-10-097-065-17
; Sequence 17, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
;  APPLICANT: Moore, Paul A. et al.
;  TITLE OF INVENTION: 110 Human Secreted Proteins
;  FILE REFERENCE: PZ021P1
;  CURRENT APPLICATION NUMBER: US/10/097,065
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: PCT/US98/27059
;  PRIOR FILING DATE: 1998-12-17
;  PRIOR APPLICATION NUMBER: 60/070,923
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,007
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,057
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,006
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,369
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,367
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,368
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,169
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,053
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,064
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,054
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,008
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,365
;  PRIOR FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 1432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-097-065-17

  Query Match             98.3%;  Score 627;  DB 15;  Length 1432;
  Best Local Similarity   99.8%;  Pred. No. 7.6e-183;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 128

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 188

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 248

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 308

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 368

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 428

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 488

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 548

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 608

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 668

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        669 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 707


RESULT 513
```

```
US-09-892-877-22
; Sequence 22, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et. al.
;  TITLE OF INVENTION: 97 Human secreted proteins
;  FILE REFERENCE: PZ028P1
;  CURRENT APPLICATION NUMBER: US/09/892,877
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 1447
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-892-877-22

  Query Match             98.2%;  Score 626.6;  DB 10;  Length 1447;
  Best Local Similarity   99.7%;  Pred. No. 1e-182;
  Matches  637;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 136

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 556

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 715


RESULT 514
US-09-948-783-22
; Sequence 22, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et. al.
;  TITLE OF INVENTION: 97 Human secreted proteins
;  FILE REFERENCE: PZ028P2
;  CURRENT APPLICATION NUMBER: US/09/948,783
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,846
;  PRIOR FILING DATE: 2000-09-11
;  PRIOR APPLICATION NUMBER: 09/892,877
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: 09/437,658
;  PRIOR FILING DATE: 1999-11-10
;  PRIOR APPLICATION NUMBER: PCT/US99/09847
;  PRIOR FILING DATE: 1999-05-06
;  PRIOR APPLICATION NUMBER: 60/085,093
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,094
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,105
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,180
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,927
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,906
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,924
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,922
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,921
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,923
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,925
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,928
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,920
;  PRIOR FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 465
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 1447
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-948-783-22

  Query Match             98.2%;  Score 626.6;  DB 10;  Length 1447;
  Best Local Similarity   99.7%;  Pred. No. 1e-182;
  Matches  637;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 136

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
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Db        377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 556

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 715
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RESULT 515
US-09-903-190-27
; Sequence 27, Application US/09903190
; Publication No. US20030162176A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/903,190
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/247,155A
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-903-190-27

Query Match 98.0%; Score 625; DB 10; Length 848;
Best Local Similarity 99.2%; Pred. No. 2.3e-182;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 516
US-10-319-763-27
; Sequence 27, Application US/10319763
; Publication No. US20030144490A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: G-031.US04.DIV
; CURRENT APPLICATION NUMBER: US/10/319,763
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-10-319-763-27

Query Match 98.0%; Score 625; DB 15; Length 848;
Best Local Similarity 99.2%; Pred. No. 2.3e-182;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 517
US-10-372-876-122
; Sequence 122, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1231)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-372-876-122

Query Match 96.4%; Score 615; DB 13; Length 1356;
Best Local Similarity 99.7%; Pred. No. 3.8e-179;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        198 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGA-G 256

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        557 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 616

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
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RESULT 518
US-10-097-065-122
; Sequence 122, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/097,065

; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1231)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-097-065-122

Query Match 96.4%; Score 615; DB 15; Length 1356;
Best Local Similarity 99.7%; Pred. No. 3.8e-179;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         18 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 77

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         78 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 137

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        198 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGA-G 256

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Db        317 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 376

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        377 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 436
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Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        437 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 496

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Job time : 346.337 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 10:39:20 ; Search time 1611.72 Seconds
(without alignments)
11820.943 Million cell updates/sec

Title: US-09-989-724-386_COPY_7_644
Perfect score: 638
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: em_gss_hum:*
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25: em_gss_rod:*
26: em_gss_phg:*
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28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	627	98.3	669	29	AY399636	AY399636 Homo sapi
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3	622.4	97.6	792	12	BG400845	BG400845 602464068
4	619.4	97.1	663	14	CB139945	CB139945 K-EST0193
5	609	95.5	639	14	CB137859	CB137859 K-EST0190
6	605.2	94.9	866	12	BG429618	BG429618 602501304
7	604	94.7	855	12	BG427247	BG427247 602494304
8	599.8	94.0	804	12	BG429705	BG429705 602493709
9	598	93.7	780	12	BG429174	BG429174 602498032
10	593	92.9	791	12	BG400319	BG400319 602464526
11	591.6	92.7	850	12	BG430955	BG430955 602500255
12	586	91.8	808	12	BG399473	BG399473 602441206
13	585.8	91.8	736	12	BG399402	BG399402 602441161
14	584.8	91.7	859	12	BG427839	BG427839 602501524
15	584.4	91.6	677	12	BG427745	BG427745 602497114
16	584.4	91.6	782	12	BG433974	BG433974 602497274
17	580.2	90.9	978	12	BI762437	BI762437 603048828
18	577	90.4	607	14	CB125058	CB125058 K-EST0173
19	576	90.3	888	12	BG400513	BG400513 602464748
20	571.4	89.6	1081	12	BM811234	BM811234 AGENCOURT
21	562	88.1	678	12	BG429011	BG429011 602501924
22	549	86.1	602	12	BG432624	BG432624 602500789
23	546.2	85.6	801	12	BG428217	BG428217 602498872
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ALIGNMENTS

RESULT 1
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LOCUS AY399636 669 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY399636
VERSION AY399636.1 GI:39755625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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gene <1. .>669
/locus_tag="HCM0290"
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Query Match 98.3%; Score 627; DB 29; Length 669;
Best Local Similarity 99.8%; Pred. No. 1.6e-163;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||||||||||||||||||||||||
Db        601 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 639
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RESULT 2
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LOCUS BI760941 870 bp mRNA linear EST 25-SEP-2001
DEFINITION 603043142F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183554 5', mRNA sequence.
ACCESSION BI760941
VERSION BI760941.1 GI:15752519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: c column: 11
High quality sequence stop: 844.
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/clone="IMAGE:5183554"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
ORIGIN

Query Match 97.6%; Score 623; DB 12; Length 870;
Best Local Similarity 99.8%; Pred. No. 2.2e-162;
Matches 634; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db         12 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 71

Qy         65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 131

Qy        125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 191

Qy        185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 251

Qy        245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 311

Qy        305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 371

Qy        365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 431

Qy        425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 491

Qy        485 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 551

Qy        545 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 611

Qy        605 ACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||| ||||||||||||||||||||||||
Db        612 ACATGAAGGGAGGGCATATTAATGATGCCTTCATG 646
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RESULT 3
BG400845
LOCUS BG400845 792 bp mRNA linear EST 12-MAR-2001
DEFINITION 602464068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592296 5', mRNA sequence.
ACCESSION BG400845

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VERSION     BG400845.1  GI:13294293
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 792)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1330  row: g  column: 17
            High quality sequence stop: 784.
FEATURES             Location/Qualifiers
     source          1. .792
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4592296"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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Query Match 97.6%; Score 622.4; DB 12; Length 792;
Best Local Similarity 99.4%; Pred. No. 3.2e-162;
Matches 636; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG---GGGCATATTAATGATGCCTTCAT 637
              ||||||||||||||   || ||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGCGGCCATATTAATGATGCCTTCAT 671
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RESULT 4
CB139945
LOCUS       CB139945                663 bp    mRNA    linear   EST 29-JAN-2003
DEFINITION  K-EST0193043 L4SNU368s1 Homo sapiens cDNA clone L4SNU368s1-5-H10
            5', mRNA sequence.
ACCESSION   CB139945
VERSION     CB139945.1  GI:28113403
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 5  row: H  column: 10
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L4SNU368s1-5-H10"
                     /sex="M"
                     /tissue_type="Liver"
                     /cell_type="Polygonal"
                     /cell_line="SNU-368"
                     /lab_host="Top10F'"
                     /clone_lib="L4SNU368s1"
                     /note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including
                     EcoRI site by treatment of T4 RNA ligase and the first
                     strand cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
                     sequencing about 2,000 - 3,000 colonies in original cDNA
```

library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

Query Match 97.1%; Score 619.4; DB 14; Length 663;
Best Local Similarity 99.7%; Pred. No. 2.1e-161;
Matches 631; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 510

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 570

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 630

Qy        601 CTGGACATG-AAGGGGGGCATATTAATGATGCC 632
              ||||||||| |||| ||||||||||||||||||
Db        631 CTGGACATGAAAGGAGGGCATATTAATGATGCC 663
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RESULT 5
CB137859
LOCUS CB137859 639 bp mRNA linear EST 29-JAN-2003
DEFINITION K-BST0190636 L4SNU368s1 Homo sapiens cDNA clone L4SNU368s1-11-F08 5', mRNA sequence.
ACCESSION CB137859
VERSION CB137859.1 GI:28108763
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 639)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 11 row: P column: 08
High quality sequence stop: 639.
FEATURES Location/Qualifiers
source 1. .639
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L4SNU368s1-11-F08"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-368"
/lab_host="Top10F'"
/clone_lib="L4SNU368s1"
/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

Query Match 95.5%; Score 609; DB 14; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.7e-158;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210
Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270
Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330
Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390
Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450
Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
Db        451 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 510
Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
Db        511 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 570
Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
Db        571 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 630
Qy        601 CTGGACATG 609
Db        631 CTGGACATG 639
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```
RESULT 6
BG429618
LOCUS       BG429618                 866 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602501304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614937 5',
            mRNA sequence.
ACCESSION   BG429618
VERSION     BG429618.1  GI:13336124
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1367  row: g  column: 02
            High quality sequence stop: 707.
FEATURES             Location/Qualifiers
     source          1. .866
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4614937"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
```

Query Match 94.9%; Score 605.2; DB 12; Length 866;
Best Local Similarity 99.1%; Pred. No. 2e-157;
Matches 630; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

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Qy          5 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 64
Db         35 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 94
Qy         65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
Db         95 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 154
Qy        125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
Db        155 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 214
Qy        185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
Db        215 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 274
Qy        245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
Db        275 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 334
Qy        305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
Db        335 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 394
Qy        365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
Db        395 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 454
Qy        425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
Db        455 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 514
Qy        485 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 544
Db        515 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 574
Qy        545 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 604
Db        575 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGAT-CCCTGG 633
Qy        605 ACATGAAGGG--GGGCATATTAATGATGCCTTCATG 638
Db        634 ACATGACGGGCAGGGCATATTATTGATGGCTTCATG 669
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RESULT 7
BG427247
LOCUS       BG427247                 855 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602494304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608048 5',
            mRNA sequence.
ACCESSION   BG427247
VERSION     BG427247.1  GI:13333753
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
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  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1349  row: h  column: 01
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4608048"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             94.7%;  Score 604;  DB 12;  Length 855;
  Best Local Similarity   99.5%;  Pred. No. 4.3e-157;
  Matches  637;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    3;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 92

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 152

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 212

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 272

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 332

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 392

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 452

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        453 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 512

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAC-AAAGAACCATCTGAAGTGGA 539
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        513 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAAGAACCATCTGAAGTGGA 572

Qy        540 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        573 TGACGCTGAAGAT-AGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 631

Qy        600 CCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        632 CCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 671


RESULT 8
BG429705
LOCUS       BG429705                 804 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602493709F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4607499 5',
            mRNA sequence.
ACCESSION   BG429705
VERSION     BG429705.1  GI:13336211
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1348  row: a  column: 04
            High quality sequence stop: 731.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4607499"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             94.0%;  Score 599.8;  DB 12;  Length 804;
  Best Local Similarity   97.2%;  Pred. No. 6.3e-156;
  Matches  621;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAG-AAAGAACAAAGAACCATCTGAAGTGGA 539

Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGCAAAGAACAAAGAACCATCTGAAGTGGA 571

Qy        540 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599

Db        572 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGACAAATGGCATCCCTCTGATCC 631

Qy        600 CCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638

Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 9
BG429174

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LOCUS       BG429174                 780 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602498032F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612062 5',
            mRNA sequence.
ACCESSION   BG429174
VERSION     BG429174.1  GI:13335680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1359  row: o  column: 07
            High quality sequence stop: 718.
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4612062"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match            93.7%;  Score 598;  DB 12;  Length 780;
  Best Local Similarity  99.8%;  Pred. No. 2e-155;
  Matches  609;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         30 TGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAG 89

Db          1 TGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAG 60

Qy         90 TATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTT 149

Db         61 TATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTT 120

Qy        150 CAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 209

Db        121 CAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 180

Qy        210 CCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCC 269

Db        181 CCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCC 240

Qy        270 TTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329

Db        241 TTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 300

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389

Db        301 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 360

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449

Db        361 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 420

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509

Db        421 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 480

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGAT 569

Db        481 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGAT 540

Qy        570 CACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGA 628

Db        541 CACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGA 600

Qy        629 TGCCTTCATG 638

Db        601 TGCCTTCATG 610
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RESULT 10
BG400319

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LOCUS       BG400319                 791 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602464526F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592575 5',
            mRNA sequence.
ACCESSION   BG400319
VERSION     BG400319.1  GI:13293767
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 791)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1331 row: c column: 08
High quality sequence stop: 711.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4592575"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 92.9%; Score 593; DB 12; Length 791;
Best Local Similarity 99.4%; Pred. No. 4.9e-154;
Matches 637; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450

Qy        421 CCCATCTGGATTATTATATTT-GGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 479
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Db        451 CCCATCTGGATTATTATATTTCGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 510

Qy        480 ACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGA 539
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Db        511 ACTGA-TTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGA 569

Qy        540 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599
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Qy        600 CCTGGACATGAAGGG-GGGCATATTAA-TGATGCCTTCATG 638
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Db        630 CCTGGACATGAAGGGAGGGCATATTAAGTGATGCCTTCATG 670
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RESULT 11
BG430955
LOCUS BG430955 850 bp mRNA linear EST 14-MAR-2001
DEFINITION 602500255F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613965 5', mRNA sequence.
ACCESSION BG430955
VERSION BG430955.1 GI:13337461
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1364 row: n column: 14
High quality sequence stop: 681.

FEATURES Location/Qualifiers
source 1. .850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4613965"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 92.7%; Score 591.6; DB 12; Length 850;
Best Local Similarity 97.5%; Pred. No. 1.2e-153;
Matches 622; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 95

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 155

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 215

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 275

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        276 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 335

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db        336 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 395

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        396 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 455

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        456 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 515

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        516 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 575

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        576 GACGCTGAAGAT-AGTGTGAAAACATGATCACAATTGAAAAATGGAT-CCCTCTGATCCC 633

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 638

Db        634 TGGACATGAAGGGAGGGCATATTACTGATGCCTTCATG 671
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RESULT 12
BG399473
LOCUS       BG399473                 808 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602441206F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557073 5',
            mRNA sequence.
ACCESSION   BG399473
VERSION     BG399473.1  GI:13293021
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 808)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1260  row: 1  column: 02
            High quality sequence stop: 637.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4557073"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
```

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ORIGIN

  Query Match            91.8%;  Score 586;  DB 12;  Length 808;
  Best Local Similarity  96.5%;  Pred. No. 4.4e-152;
  Matches  610;  Conservative    0;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGT--GTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATC 598

Db        572 GACGCTGAAGATAAGTTGTTGAAAACATGATCCCAATCTGAAATGGGCTTCCCTCTGATC 631

Qy        599 CCCTGGACATGAAGGGGGGCATATTAATGATG 630

Db        632 CCCTGGACCTGAAGAGGAGGGCCTATTTAATG 663
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RESULT 13
BG399402
LOCUS       BG399402                 736 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602441161F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557015 5',
            mRNA sequence.
ACCESSION   BG399402
VERSION     BG399402.1  GI:13292850
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1260 row: i column: 16
High quality sequence stop: 661.

FEATURES Location/Qualifiers
source 1. .736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4557015"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 91.8%; Score 585.8; DB 12; Length 736;
Best Local Similarity 99.2%; Pred. No. 4.9e-152;
Matches 620; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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Qy          12 GCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGC 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           3 GCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGC 62

Qy          72 TTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATAC 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 TTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATAC 122

Qy         132 CAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAG 191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 CAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAG 182

Qy         192 AGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTG 251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         183 AGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTG 242

Qy         252 GTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGC 311
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 GTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGC 302

Qy         312 CATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGA 371
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 CATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGA 362

Qy         372 ATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGAT 431
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         363 ATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGAT 422

Qy         432 TATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATC 491
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         423 TATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATC 482

Qy         492 AGGGATCTGGCAACGTAGAAG-AAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAG 550
               |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         483 AGGGATCTGGCAACGTAGAAGAAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAG 542

Qy         551 ATAAGTGTGAAAACATGATCACAA-TTGAAAATGGCATCCCCTCTGATCCCCTGGACATG 609
               |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db         543 ATAAGTGTGAAAACATGATCACAATTTGAAAATGGCATCCCCTCTGAT-CCCTGGACATG 601

Qy         610 AAGGGGGGCATATTAATGATGCCTT 634
               | || ||||||||||||||||||||
Db         602 AGGGAGGGCATATTAATGATGCCTT 626
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RESULT 14
BG427839
LOCUS BG427839 859 bp mRNA linear EST 14-MAR-2001
DEFINITION 602501524F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4615156 5', mRNA sequence.
ACCESSION BG427839
VERSION BG427839.1 GI:13334345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1367 row: p column: 05
High quality sequence stop: 661.

FEATURES Location/Qualifiers
source 1. .859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4615156"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 91.7%; Score 584.8; DB 12; Length 859;
Best Local Similarity 99.2%; Pred. No. 9.5e-152;
Matches 619; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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Qy          14 TCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTT 73
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 TCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTT 61

Qy          74 TTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCA 133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCA 121

Qy         134 ATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAG 193
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 ATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAG 181

Qy         194 AAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGT 253
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 AAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGT 241

Qy         254 TTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCA 313
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 TTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCA 301

Qy         314 TAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAAT 373
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Qy          374 TTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTA 433
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Qy          434 TTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAG 493
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Qy          494 GGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATA 553
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Qy          554 AGTGTGAAAACATGATCACAATTGAAAA-TGGCATCCCCTCTGATCCCCT-GGACATGAA 611
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Db          542 AGTGTGAAAACATGATCACAATTGAAAATTGGCATCGCCTCTGATCCCCTGGGACATGAA 601

Qy          612 GGG-GGCATATTAATGATGCCTT 634
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Db          602 GGGAGGGCATATTAATGATGCCCT 625
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RESULT 15
BG427745

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LOCUS       BG427745                677 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602497114F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4610834 5',
            mRNA sequence.
ACCESSION   BG427745
VERSION     BG427745.1  GI:13334251
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1356  row: 1  column: 03
            High quality sequence stop: 677.
FEATURES             Location/Qualifiers
     source          1. .677
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                     /clone="IMAGE:4610834"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             91.6%;  Score 584.4;  DB 12;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-151;
  Matches  629;  Conservative    0;  Mismatches    2;  Indels    4;  Gaps    4;

Qy            5 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 64
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           36 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 95

Qy           65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           96 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 155

Qy          125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          156 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 215

Qy          185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          216 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 275

Qy          245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          276 CATTCTGGTNTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 335

Qy          305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
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Db          336 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 395

Qy          365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          396 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 455

Qy          425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
                |||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||
Db          456 TCTGGATTATTATATTCGGTGTGATA-TTTGCATCATCATAGTTGCAATTGCACTACTGA 514

Qy          485 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 544
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db          515 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA-CATCTGAAGTGGATGACG 573

Qy          545 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 604
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db          574 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGG-ATCCCCTCTGATCCCCTGG 632

Qy          605 ACATGAAGGG-GGCATATTAATGATGCCTTCATG 638
                |||||||||| ||||||||||||||||||||||||
Db          633 ACATGAAGGGAGGGCATATTAATGATGCCTTCATG 667
```

RESULT 16
BG433974

```
LOCUS       BG433974                782 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602497274F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4611018 5',
            mRNA sequence.
ACCESSION   BG433974
VERSION     BG433974.1  GI:13340480
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 782)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1357  row: c  column: 19
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High quality sequence stop: 701.

FEATURES Location/Qualifiers
source 1. .782
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4611018"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 91.6%; Score 584.4; DB 12; Length 782;
Best Local Similarity 98.4%; Pred. No. 1.2e-151;
Matches 632; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGAATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCATCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGAT-AAGTGTGAAAACATGATCACAATTGA-AAATGGCATCCCCTCTGA-T 597
              |||||||||||| |||||||| | ||||||||| ||||| |||||| |||||||||| |
Db        572 GACGCTGAAGATCAAGTGTGACACCATGATCACCATTGACAAATGGGATCCCCTCTGAGT 631

Qy        598 CCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||||| |||||||||||||||||||||||
Db        632 CCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 673
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RESULT 17
BI762437
LOCUS BI762437 978 bp mRNA linear EST 25-SEP-2001

DEFINITION 603048828F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189023 5', mRNA sequence.
ACCESSION BI762437
VERSION BI762437.1 GI:15754015
KEYWORDS BST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11472 row: g column: 08
High quality sequence stop: 826.

FEATURES Location/Qualifiers
source 1. .978
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5189023"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 90.9%; Score 580.2; DB 12; Length 978;
Best Local Similarity 98.7%; Pred. No. 1.9e-150;
Matches 604; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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Qy         29 CTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTA 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTA 60

Qy         89 GTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCT 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCT 120

Qy        149 TCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTT 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTT 180

Qy        209 CCCA-TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGAC 267
              |||| |||||||| ||||||||||||||||||||||||||||| ||||||||||||||
Db        181 CCCAGTGTCCTACTNTGCAATGTAACCCAGAGGGTATCATTCTGGTGTGTGGTTACAGAC 240

Qy        268 CCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAG 327
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        241 CCTTCAAAAAATCACACCCTTCCTGCTGNTGAGGTGCAATCAGCCATAAGAATGAACAAG 300

Qy        328 AACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCT 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCT 360
```

```
Qy        388 TCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        361 TCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATNTGGTGTG 420

Qy        448 ATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGT 507
              |||||| |||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        421 ATATTTGGCATCATCATAGTTGCAATGGCACTACTGATTTTATCAGGGATCTGGCAACGT 480

Qy        508 AGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATG 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATG 540

Qy        568 ATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAAT 626
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        541 ATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAAT 600

Qy        627 GATGCCTTCATG 638
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Db        601 GATGCCTTCATG 612
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RESULT 18
CB125058
LOCUS CB125058 607 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0173841 L4SNU368s1 Homo sapiens cDNA clone L4SNU368s1-3-H04 5', mRNA sequence.
ACCESSION CB125058
VERSION CB125058.1 GI:28085812
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 607)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 3 row: H column: 04
High quality sequence stop: 607.
FEATURES Location/Qualifiers
source 1. .607
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L4SNU368s1-3-H04"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-368"
/lab_host="Top10F'"
/clone_lib="L4SNU368s1"
/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

Query Match 90.4%; Score 577; DB 14; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e-149;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        451 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 510

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 570

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTG 577
              |||||||||||||||||||||||||||||||||||||
Db        571 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTG 607
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RESULT 19
BG400513
LOCUS BG400513 888 bp mRNA linear EST 12-MAR-2001
DEFINITION 602464748F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592890 5', mRNA sequence.
ACCESSION BG400513
VERSION BG400513.1 GI:13293961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 888)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1331 row: p column: 11
High quality sequence stop: 723.
FEATURES Location/Qualifiers
source 1. .888
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4592890"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 90.3%; Score 576; DB 12; Length 888;
Best Local Similarity 97.7%; Pred. No. 2.7e-149;
Matches 627; Conservative 0; Mismatches 10; Indels 5; Gaps 4;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 95

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTA-GTATCAGAACAGCTCTGGGAGATAAAGCATA 119
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         96 GCAGAAAATGCTTTTAAAGTGAGACTTATGTATCAGAACAGCTCTGGGAGATAAAGCATA 155

Qy        120 TGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 TGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 215

Qy        180 AGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAG 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 AGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAG 275

Qy        240 GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGA 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 GGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGA 335

Qy        300 GGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGA 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGA 395

Qy        360 CCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGT 419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGT 455

Qy        420 GCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 479
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 515
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Qy        480 ACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGA 539
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        516 ACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAAACATCTGAAGTGGA 575

Qy        540 TGACGCTG-AAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATC 598
              |||||||| |||||||||||||||| |||||||||||||||||| || ||||||||||
Db        576 TGACGCTGCAAGATAAGTGTGAAAAACTGATCACAATTGAAAATGGGAT-CCCTCTGATC 634

Qy        599 CCCTGGACATGAAGG--GGGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| ||| ||| ||||||||||||||
Db        635 CCCTGGACATGAAGGGAGGGCATATTTATTGATGCCTTCATG 676
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RESULT 20
BM811234
LOCUS BM811234 1081 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6489717 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723829 5', mRNA sequence.
ACCESSION BM811234
VERSION BM811234.1 GI:19128057
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1081)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12712 row: b column: 22
High quality sequence stop: 721.
FEATURES Location/Qualifiers
source 1. .1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5723829"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
ORIGIN

Query Match 89.6%; Score 571.4; DB 12; Length 1081;
Best Local Similarity 99.7%; Pred. No. 5.3e-148;
Matches 583; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy         55 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 114
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 CGAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 224

Qy        115 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 174
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 284

Qy        175 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 234
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Db        285 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 344

Qy        235 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 404

Qy        295 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 464

Qy        355 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 524

Qy        415 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 584

Qy        475 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 644

Qy        535 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 704

Qy        595 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||||||||||| ||||||||||||||||||||||||
Db        705 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 749
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RESULT 21
BG429011

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LOCUS       BG429011                678 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602501924F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4615540 5',
            mRNA sequence.
ACCESSION   BG429011
VERSION     BG429011.1  GI:13335517
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1368  row: p  column: 05
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1. .678
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4615540"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match           88.1%;  Score 562;  DB 12;  Length 678;
  Best Local Similarity  96.7%;  Pred. No. 2e-145;
  Matches  615;  Conservative    0;  Mismatches   17;  Indels    4;  Gaps    4;

Qy          5 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 93

Qy         65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 153

Qy        125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 213

Qy        185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 273

Qy        245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
              |||||||| ||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        274 CATTCTGGTNTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTNGAGGTGC 333

Qy        305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 393

Qy        365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 453

Qy        425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 513

Qy        485 TTTTATCAGGGATC-TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGAC 543
              |||||||||||||| |||||||||||||||||||||||||| ||||||||||||||||
Db        514 TTTTATCAGGGATCTTGGCAACGTAGAAGAAAGAACAAAGAA-CATCTGAAGTGGATGA- 571

Qy        544 GCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTG 603
              |||||||||||||||||||||||||||||||||||||||||||    |||        ||| ||
Db        572 GCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGATCCCCTCTGATCCCCGTG 631

Qy        604 GACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              |||||||||||| |||||||||||||||||| |  ||
Db        632 GACATGAAGGGAGGGCATATTAATGATGCTTCATTG 667
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RESULT 22
BG432624

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LOCUS       BG432624                  602 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602500789F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614070 5',
            mRNA sequence.
ACCESSION   BG432624
VERSION     BG432624.1  GI:13339130
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
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            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1365  row: b  column: 23
           High quality sequence stop: 602.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4614070"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             86.1%;  Score 549;  DB 12;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 8.3e-142;
  Matches  571;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATA-TTGGTGTGATA-TTTGCATCATCATAGTTGCAATTGCACTA 509

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        510 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 569

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACA 573
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Db        570 GACGCTGAAGATAAGTGTGAAAACATGATCACA 602
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RESULT 23
BG428217
LOCUS       BG428217                 801 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602498872F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612840 5',
            mRNA sequence.
ACCESSION   BG428217
VERSION     BG428217.1  GI:13334723
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1361  row: o  column: 17
           High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .801
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4612840"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             85.6%;  Score 546.2;  DB 12;  Length 801;
  Best Local Similarity   96.6%;  Pred. No. 5.3e-141;
  Matches  623;  Conservative    0;  Mismatches   13;  Indels    9;  Gaps    6;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 140

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 200

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 260

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 320

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        321 GTATCATTCTGGTTGGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 380

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        381 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 440

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 500

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              |||||||||||||| |||||| |||||||||||| ||||||||||||||||||||||||
Db        501 CCCATCTGGATTA-TATATTGGGTGTGATATTTGGCATCATCATAGTTGCAATTGCACTA 559

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAA---GAAAGAACAAAGAACCATCTGAAGTG 537
              |||| |||||||||||||||||||||||| |   | ||||||||||||||||||||||
Db        560 CTGA-TTTATCAGGGATCTGGCAACGTAGCAACGAACGGAACAAAGAACCATCTGAAGTG 618

Qy        538 GATGACGCTGAAGAT-AAGTGTGAAAACATGATCACAATTGA-AAATGGCATCCCCTCTG 595
              ||||||||||||||| | |||||||||||||||||||||||| |||||| ||||||||||
Db        619 GATGACGCTGAAGATCACGTGTGAAAACATGATCACAATTGACAAATGGAATCCCCTCTG 678

Qy        596 ATCCCCTGGACATGAA--GGGGGGCATATTAATGATGCCTTCATG 638
              ||| |||||||||| ||  || |||||| ||||||||||||||||
Db        679 ATCGCCTGGACATTAAAGGGAGGGCATCTTAATGATGCCTTCATG 723
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RESULT 24
BG399975
LOCUS BG399975 884 bp mRNA linear EST 12-MAR-2001
DEFINITION 602442028F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557751 5', mRNA sequence.
ACCESSION BG399975
VERSION BG399975.1 GI:13293423
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1262 row: h column: 08
High quality sequence stop: 590.
FEATURES Location/Qualifiers
source 1. .884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4557751"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 85.6%; Score 546.2; DB 12; Length 884;
Best Local Similarity 94.6%; Pred. No. 5.4e-141;
Matches 599; Conservative 0; Mismatches 28; Indels 6; Gaps 3;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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RESULT 25
AV653898
LOCUS AV653898 735 bp mRNA linear EST 15-JAN-2002
DEFINITION AV653898 GLC Homo sapiens cDNA clone GLCDPG08 3', mRNA sequence.
ACCESSION AV653898
VERSION AV653898.1 GI:9874912
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 735)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919(ex.45)

```
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
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ORIGIN

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  Matches  574;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    3;

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Db        121 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 180

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Db        361 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 420

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        421 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 480

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Db        541 ACTGATTNTATCAGGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGG 600

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RESULT 26
AY399637
LOCUS       AY399637                 669 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY399637
VERSION     AY399637.1  GI:39755626
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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                     /mol_type="genomic DNA"
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ORIGIN

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  Best Local Similarity  83.1%;  Pred. No. 2.2e-133;
  Matches  531;  Conservative    0;  Mismatches  107;  Indels    1;  Gaps    1;

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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Job time : 1618.72 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 10:27:09 ; Search time 57.8831 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	625	98.0	848	3	US-08-905-223-27	Sequence 27, Appl
2	625	98.0	848	4	US-09-247-155-27	Sequence 27, Appl
3	625	98.0	848	4	US-09-663-600A-27	Sequence 27, Appl
4	625	98.0	848	4	US-09-621-976-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; DEVELOPMENTAL STAGE: Fetal
; TISSUE TYPE: kidney
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 10.7
; OTHER INFORMATION: seq LWLLFFLVTAIHA/EL
US-08-905-223-27

Query Match 98.0%; Score 625; DB 3; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy  181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Qy  361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy  421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
Db  452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy  481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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RESULT 2
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATG 638
              ||||||||||||||| |||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 3
US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331
Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451
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Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATG 670
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RESULT 4
US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..697
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151
Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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